



STIC Search Report

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STIC Database Tracking Number: 178070

TO: Manjunath N Rao
Location: rem/2A01/2C70
Art Unit: 1652
Tuesday, February 07, 2006
Case Serial Number: 10/626583

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

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178070 me

STIC-Biotech/ChemLib

From: Rao, Manjunath N.
Sent: Tuesday, January 31, 2006 8:22 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request for 10626583

From: Manjunath N. Rao
Art Unit 1652, Room 2A01
Mail Box in Room 2C70
Phone: 272-0939

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Date: 1-31-06

Please search the following as soon as possible for application with serial number
10/626583

1. **SEQ ID NO: 5** against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.

If you have any questions please call me at the above phone number.

Thanks

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s).
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:14:02 ; Search time 93 Seconds
(without alignments)
1006.319 Million cell updates/sec

Title: US-10-626-583-5
Perfect score: 1171
Sequence: 1 MFKFKPLVGLSAAALMSIS.....YQVMATEGYQSSGSNTVTW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	3	AAY93752 A bacteri
2	1171	100.0	213	7	ADC27541 Bacillus
3	1171	100.0	213	7	ADO55909 Bacillus
4	1171	100.0	213	8	ADJ34972 Xylanase
5	1168	99.7	213	3	AB48532 Bacillus
6	1168	99.7	213	3	AB48518 Bacillus
7	1168	99.7	213	5	AAO18638 B subtili
8	1168	99.7	213	5	AAO18624 Endo-1,4-
9	1168	99.7	213	8	ADJ35008 Xylanase
10	1168	99.7	213	8	ADI66728 B. circul
11	1168	99.7	213	8	ADI66740 B. subtil
12	1161	99.1	213	3	AAY93755 A bacteri
13	1154	98.5	213	3	AAY93753 A bacteri
14	1149	98.1	213	3	AAY93754 A bacteri
15	1130	96.5	213	2	AAR47200 Modified
16	1130	96.5	213	3	AAY93751 A bacteri
17	1125	96.1	213	8	ADO70164 Xylanase,
18	1104	94.3	213	8	ADJ35014 Xylanase
19	1097	93.7	213	8	ADJ35086 Xylanase
20	1041	88.9	185	2	AAW60732 Xylanase
21	1041	88.9	185	3	AAV98064 B. subtil
22	1041	88.9	185	4	AB485043 B. subtil
23	1041	88.9	185	4	AAU07391 Bacillus
24	1041	88.9	185	5	AAE18441 Bacillus

25	1041	88.9	185	7	ADC27530 Bacillus
26	1041	88.9	197	8	ADH10230 Xylanase
27	1041	88.9	353	4	AB485045 Xylanase
28	1041	88.9	360	8	ADH10231 Xylanase
29	1038	88.6	185	2	AAW60730 Xylanase
30	1038	88.6	185	3	AAV98062 B. circul
31	1038	88.6	185	5	AAO18625 B. circula
32	1038	88.6	185	5	AAE18439 Bacillus
33	1034	88.3	353	4	AB485046 ND-xylana
34	1033	88.2	185	2	AAW60279 Modified
35	1030	88.0	185	2	AAW60278 Modified
36	987	84.3	185	3	AB48524 Xylanase
37	987	84.3	185	3	AB48523 Xylanase
38	987	84.3	185	5	AAO18629 Modified
39	987	84.3	185	5	AAO18630 Modified
40	987	84.3	185	8	ADI66732 B. circul
41	984	84.0	185	3	AB48528 Xylanase
42	984	84.0	185	5	AAO18634 Modified
43	984	84.0	185	8	ADI66736 B. circul
44	979	83.6	185	3	AB48526 Xylanase
45	979	83.6	185	5	AAO18632 Modified

ALIGNMENTS

RESULT 1
AAY93752
ID AAY93752 standard; protein; 213 AA.
XX
AC AAY93752;
XX
DT 03-OCT-2000 (first entry)
XX
DE A bacterial endo-beta-1,4-xylanase protein.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
KW dough; dough preparation.
XX
OS Bacillus subtilis.
PN WO200039289-A2.
XX
PD 06-JUL-2000.
XX
PF 17-DEC-1999; 99WO-IB002071.
XX
PR 23-DEC-1998; 98GB-00028599.
PR 06-APR-1999; 99GB-00007805.
PR 15-APR-1999; 99GB-00008645.
(DANI-) DANISCO AS.
Sibbesen O, Sorensen JF;
WPI; 2000-465744/40.
N-PSDB; AAA47154.
Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.
Claim 10; Page 108; 112pp; English.
The present sequence represents an endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the

inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample

Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-91;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNTSVNWSN 60
Db 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNTSVNWSN 60

Qy 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLIEYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLIEYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSNAITTSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSNAITTSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 2
ADC27541
ID ADC27541 standard; protein; 213 AA.
XX
AC ADC27541;
XX
DT 18-DEC-2003 (first entry)
XX
DE Bacillus subtilis wild-type xylanase enzyme.
XX
KW xylanase; xylanase inhibitor; thermosensitivity; plant cell wall;
KW plant material; baking; processing cereal; starch production;
KW processing wood; wood pulp bleaching; animal feed; flour separation;
KW wetmilling; paper and pulp production; flour dough; hemicellulose;
KW arabinoxylan; food supplement; xylan; baking process; bread volume;
KW crumb structure; crumb appearance; shelf-life; enzyme.
XX
OS Bacillus subtilis.
XX
PN WO2003020923-A1.
XX
XX 13-MAR-2003.
XX
PF 30-AUG-2002; 2002MO-IB003797.
XX
PR 04-SEP-2001; 2001GB-00021387.
XX
PA (DANI-) DANISCO AS.
XX
PI Sibbesen O, Sorensen JF;
XX
XX WPI; 2003-332934/31.
DR N-PSDB; ADC27538.
XX
XX Novel variant xylanase polypeptide having altered sensitivity to a
PT xylanase inhibitor and altered thermosensitivity as compared with a
PT parent xylanase enzyme, useful in baking, processing cereals, starch
PT production.
PS
PS Disclosure; Fig 1; 63pp; English.
XX
XX This invention relates to a novel variant xylanase protein or its
CC fragment having xylanase activity. the variants have one or more amino
CC acid modifications so that the protein or fragment has an altered
CC sensitivity to a xylanase inhibitor and has an altered thermosensitivity
CC as compared with a parent xylanase enzyme. The variant xylanases of the
CC invention are useful for degrading or modifying a plant cell wall, and

for processing a plant material. They may be useful for baking, processing cereals, starch production, in processing wood, and enhancing the bleaching of wood pulp. They may also be useful for a variety of applications such as animal feed, flour separation (wetmilling) and paper and pulp production. In addition, they may also be useful for preparing a flour dough. The enzymes of the invention may alter or reduce the viscosity derived from the presence of hemicellulose or arabinoxylan in a solution or system comprising plant cell wall material, and for modifying food and/or feed supplement comprising xylan. Use of the variant xylanases in baking processes improves the properties of flour based doughs and products made from the doughs. The baked products have highly desirable characteristics with respect to blood volume, crumb structure and appearance and additionally have an extended shelf-life. The enzymes of the invention have reduced thermosensitivity and inhibitor sensitivity, which allows a reduction in the amount of xylanase required for animal feed, starch production and baking. The present sequence is that of the full-length wild-type Bacillus subtilis xylanase which was used to create the variant xylanases of the invention.

Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-91;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNTSVNWSN 60
Db 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNTSVNWSN 60

Qy 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLIEYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTSPLIEYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSNAITTSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSNAITTSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 3
ADO55909
ID ADO55909 standard; protein; 213 AA.
XX
AC ADO55909;
XX
XX 15-JUL-2004 (first entry)
XX
DE Bacillus subtilis xynA protein sequence SeqID4.
XX
KW cellulase; microorganism; organic fertilizer; faeces; urine;
KW domestic animal; sawdust; pLYH7-39; bglc; xylanase; pLYH8-49; xynA;
KW pLYH8-62; xynD; pectate lyase; pLYH9-24; pella; pLYH9-46; pella;
KW fermentation; enzyme.
XX
OS Bacillus subtilis.
XX
XX KR2003015943-A.
XX
XX 26-FEB-2003.
XX
XX 18-AUG-2001; 2001KR-00049794.
PF
PR 18-AUG-2001; 2001KR-00049794.
XX
XX (KOBI-) KOREA BIO FERTILIZER CO LTD.
XX
PI Lee YH, Yoon HJ;
XX
DR WPI; 2003-455433/43.
DR N-PSDB; ADO55908.

XX Gene encoding cellulase, cellulase expressed by the same, microorganism
 PT containing the same gene, and organic fertilizer using the same
 PT microorganism.
 XX
 PS Claim 2; SEQ ID NO 4; 1pp; Korean.
 XX
 CC This invention relates to novel genes encoding cellulase, cellulase
 CC expressed by the same, a microorganism containing the same gene, and an
 CC organic fertilizer using the same microorganism, therefore the organic
 CC fertilizer can be rapidly produced from a mixture of the faeces and urine
 CC of domestic animals and sawdust. The microorganism *Bacillus subtilis*
 CC contains one cellulase encoding gene pLVH7-39(bgIC), two xylanase
 CC encoding genes pLVH8-49(xyNA) and pLVH8-62(xyND) and two pectate lyase
 CC encoding genes pLVH9-24(peIA) and pLVH9-46(peIB). The organic fertilizer
 CC is produced by inoculating an appropriate amount of the microorganism
 CC *Bacillus subtilis* into the mixture of the faeces and urine of domestic
 CC animals and sawdust and fermenting the mixture. The present sequence is
 CC that of a *Bacillus subtilis* protein which is related to the production of
 CC the organic fertilizer of the invention.

XX Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60
 DB 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60
 QY 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
 DB 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
 QY 121 TYKGTVKSDDGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 DB 121 TYKGTVKSDDGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 QY 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVW 213
 DB 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVW 213

RESULT 4

ADJ34972
 ID ADJ34972 standard; protein; 213 AA.

XX AC ADJ34972;

XX DT 22-APR-2004 (first entry)

XX DE Xylanase from an environmental sample seq id 188.

XX KW antibacterial; fungicide; thermostable xylanase activity;
 KW dough conditioning; beverage production; nutritional supplement;
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
 KW fungal infection; coccidiosis.

XX OS Unidentified.

XX FN WO2003106654-A2.

XX PD 24-DEC-2003.

XX PF 16-JUN-2003; 2003WO-US019153.

XX PR 14-JUN-2002; 2002US-0389299P.

XX PA (DIVE-) DIVERSA CORP.

XX PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 PI Esteghlalian A;

PI

XX

DR WPI; 2004-099016/10.
 DR N-PSDB; ADJ34971.

XX Novel xylanase recombinant polypeptide useful for improving textile
 PT texture, treating paper, eliminating microorganisms.

XX Claim 60; SEQ ID NO 188; 570pp; English.

XX The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences
 CC (SI), given in the specification, over a region of 100 or more residues
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This is the amino acid sequence of a xylanase protein isolated from an
 CC environmental sample.

XX Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 8; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60
 DB 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60
 QY 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
 DB 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
 QY 121 TYKGTVKSDDGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 DB 121 TYKGTVKSDDGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
 QY 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVW 213
 DB 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVW 213

RESULT 5

AAB48532

ID AAB48532 standard; protein; 213 AA.

XX AC AAB48532;

XX DT 05-MAR-2001 (first entry)

XX DE *Bacillus subtilis* xylanase.

XX KW Bacterial; *Bacillus* circulans; xylanase; xylanase activity; XA;
 KW bleaching agent.

XX OS *Bacillus subtilis*.

XX FN WO200068396-A2.

XX PD 16-NOV-2000.

XX PF 12-MAY-2000; 2000WO-US013172.

XX PR 12-MAY-1999; 99US-0133714P.

XX PA (XENC-) XENCOR INC.

XX PI Bentzien JM;

XX WPI; 2000-679800/66.
XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX
XX Disclosure; Fig 16A; 114pp; English.
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 3; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 6
AAB48518
ID AAB48518 standard; protein; 213 AA.
XX
XX AAB48518;
XX
XX 05-MAR-2001 (first entry)
XX
XX Bacillus circulans endo-1,4-beta xylanase precursor.
XX
XX Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent.
XX
XX Bacillus circulans.
XX
XX WO200068396-A2.
XX
XX 16-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US013172.
XX
XX 12-MAY-1999; 99US-0133714P.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien JM;
XX
XX WPI; 2000-679800/66.
XX
XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX Disclosure; Fig 1A; 114pp; English.
XX
PS

XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 3; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 7
AAO18638
ID AAO18638 standard; protein; 213 AA.
XX
XX AAO18638;
XX
XX 24-OCT-2002 (first entry)
XX
XX B subtilis xylanase.
XX
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutain.
XX
XX Bacillus subtilis.
XX
XX WO200238746-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US048018.
XX
XX 10-NOV-2000; 2000US-00710050.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien J, Dahiyat B;
XX
XX WPI; 2002-608200/65.
XX
XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
XX Disclosure; Fig 16A; 121pp; English.
XX
XX The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC

CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60
DB 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60
QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLYGWTRSPLEYVYVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLYGWTRSPLEYVYVDSWGTYPRTG 120
QY 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 8
AAO18624
ID AAO18624 standard; protein; 213 AA.
XX AAO18624;
XX AC
XX DT 24-OCT-2002 (first entry)
XX DE Endo-1,4-beta xylanase precursor protein.
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
XX liquid clarification; coffee extraction; plant oil extraction;
XX starch extraction; food thickener; animal food additive; mutant; mutein.
XX Unidentified.
XX WO200238746-A2.
XX PN
XX PD 16-MAY-2002.
XX PF 09-NOV-2001; 2001WO-US048018.
XX PR 10-NOV-2000; 2000US-00710050.
XX PA (XENC-) XENCOR INC.
XX PI Bentzien J, Dahiyat B;
XX WPI; 2002-608200/65.
XX Novel xylanase activity protein, useful in bleaching process of pulp and
XX in food and animal feed industry, has enhanced thermostability and
XX alkalophilicity.
XX Disclosure; Fig 1A; 121pp; English.
XX The present invention relates to a non-naturally occurring xylanase
XX activity (XA) protein comprising an amino acid sequence less than 97%
XX identical to a naturally occurring Bacillus circulans xylanase, where the

CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60
DB 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60
QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLYGWTRSPLEYVYVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLYGWTRSPLEYVYVDSWGTYPRTG 120
QY 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 9
ADJ35008
ID ADJ35008 standard; protein; 213 AA.
XX AC
XX ADJ35008;
XX DT 22-APR-2004 (first entry)
XX DE Xylanase from an environmental sample seq id 224.
XX antibacterial; fungicide; thermostable xylanase activity;
XX dough conditioning; beverage production; nutritional supplement;
XX animal feed; lignin reduction; wood product; xylan; bacterial infection;
XX fungal infection; coccidioidosis.
XX Unidentified.
XX OS
XX WO2003106654-A2.
XX PN
XX PD 24-DEC-2003.
XX PF 16-JUN-2003; 2003WO-US019153.
XX PR 14-JUN-2002; 2002US-0389299P.
XX PA (DIVE-) DIVERSA CORP.
XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
XX Esteghlalian A;
XX WPI; 2004-099016/10.
XX N-PSDB; ADJ35007.
XX Novel xylanase recombinant polypeptide useful for improving textile
XX texture, treating paper, eliminating microorganisms.
XX Claim 60; SEQ ID NO 224; 570pp; English.

XX The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190-1200 residue amino acid sequences
 CC (SI), given in the specification, over a region of 100 or more residues
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This is the amino acid sequence of a xylanase protein isolated from an
 CC environmental sample.

XX Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;
 Best Local Similarity 99.5%; Pred. No. 3.3e-91;
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKQFLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60
 Db 1 MFKFKQFLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60
 Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120
 Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120
 Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
 Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 10
 ADI66728 standard; protein; 213 AA.

XX ADI66728;
 XX AC
 XX DT 22-APR-2004 (first entry)

DE B. circulans endo-1,4-beta xylanase.

XX Endo-1,4-beta xylanase; XA; EC 3.2.1.8; enzyme; bleaching;
 KW bleaching pulp; paper industry; food; animal feed; thermostability;
 KW alkalophilic; hot alkali treatment.

XX Bacillus circulans.

XX Key Location/Qualifiers
 FT Peptide 1..28
 FT /note= "Signal peptide"
 FT Protein 29..213
 FT /note= "Mature Xylanase"

XX US6682923-B1.

XX 27-JAN-2004.

XX 12-MAY-2000; 2000US-00570856.

XX 12-MAY-1999; 99US-0133714P.

XX 07-JUN-1999; 99US-0138156P.

XX (XENC-) XENCOR.

XX Bentzien J, Dahiyat BI;

XX WPI; 2004-118575/12.
 DR N-PSDB; ADI66729.

XX New mutant xylanase (XA) protein comprising at least four amino acid
 PT substitutions as compared to Bacillus circulans xylanase, useful for
 PT bleaching (paper) pulp, and in the food and animal feed industries.

XX Claim 2; SEQ ID NO 1; 84pp; English.

XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
 CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also
 CC included is a bleaching agent comprising the XA protein. The non-
 CC naturally occurring XA protein comprises at least four amino acid
 CC substitutions as compared to Bacillus circulans xylanase ADI66728. The
 CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
 CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
 CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
 CC useful for bleaching pulp in the paper and related industries, but is
 CC also useful in the food and animal feed industries. The new protein is
 CC active at higher pH and temperature ranges than naturally occurring
 CC xylanases, simplifying incorporation of the xylanase treatment step into
 CC pulp processing, especially where the enzyme is added after hot alkali
 CC treatment. The present sequence represents the wild-type xylanase.

XX Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;
 Best Local Similarity 99.5%; Pred. No. 3.3e-91;
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKQFLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60
 Db 1 MFKFKQFLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60
 Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120
 Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120
 Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
 Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 11

ADI66740
 ID ADI66740 standard; protein; 213 AA.

XX ADI66740;

XX DT 22-APR-2004 (first entry)

XX B. subtilis xylanase.

XX Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
 KW paper industry; food; animal feed; thermostability; alkalophilic;
 KW hot alkali treatment.

XX Bacillus subtilis.

XX US6682923-B1.

XX 27-JAN-2004.

XX 12-MAY-2000; 2000US-00570856.

XX 12-MAY-1999; 99US-0133714P.

XX 07-JUN-1999; 99US-0138156P.

(XENC-) XENCOR.
PA XX
XX PI Bentzien J, Dahiyat BI;
XX DR WPI; 2004-118575/12.
XX XX
XX XX
XX XX
XX PT New mutant xylanase (XA) protein comprising at least four amino acid
XX PT substitutions as compared to Bacillus circulans xylanase, useful for
XX PT bleaching (paper) pulp, and in the food and animal feed industries.
XX XX
XX PS Disclosure; SEQ ID NO 13; 84pp; English.
XX XX
XX XX
XX CC The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
XX CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also
XX CC included is a bleaching agent comprising the XA protein. The non-
XX CC naturally occurring XA protein comprises at least four amino acid
XX CC substitutions as compared to Bacillus circulans xylanase ADI66728. The
XX CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
XX CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
XX CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
XX CC useful for bleaching pulp in the paper and related industries, but is
XX CC also useful in the food and animal feed industries. The new protein is
XX CC active at higher pH and temperature ranges than naturally occurring
XX CC xylanases, simplifying incorporation of the xylanase treatment step into
XX CC pulp processing, especially where the enzyme is added after hot alkali
XX CC treatment. The present sequence is a xylanase from another species
XX CC included for comparison.
XX XX
XX SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91; Indels 0; Gaps 0;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWTDGGGIYNAVNGSGGYSVNWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWTDGGGIYNAVNGSGGYSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKPTGSGNATITFSNHVNA 180

Qy 181 WKSHGMGLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMGLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 12
AA93755
ID AAY93755 standard; protein; 213 AA.
AC AAY93755;
XX XX
XX DT 03-OCT-2000 (first entry)
XX XX
XX DE A bacterial endo-beta-1,4-xylanase mutant XM3.
XX XX
XX KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX KW dough; dough preparation.
XX OS Synthetic.
XX OS Bacillus subtilis.
XX FN WO200039289-A2.
XX XX
XX PD 06-JUL-2000.
XX XX
XX PF 17-DEC-1999; 99WO-IB002071.
XX XX

23-DEC-1998; 98GB-00028599.
06-APR-1999; 99GB-00007805.
15-APR-1999; 99GB-00008645.
XX XX
XX XX (DANI-) DANISCO AS.
XX XX
XX XX Sibbesen O, Sorensen JF;
XX PI
XX XX WPI; 2000-465744/40.
XX DR N-PSDB; AAA47157.
XX XX
XX PT Mutant xylanase protein identified using xylanase inhibitor useful for
XX PT preparing non-sticky dough for bakery products.
XX XX
XX PS Claim 1; Page 111; 112pp; English.
XX XX
XX CC The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX CC specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX CC is obtained from wheat flour. The specification also describes a mutant
XX CC xylanase protein. The xylanase is useful for preparing a foodstuff.
XX CC preferably a bakery product or a substance (e.g. a dough) for making the
XX CC bakery product. Wild type xylanase or mutant xylanase is useful for
XX CC preparing a dough that is less sticky than a dough comprising a fungal
XX CC xylanase. The xylanase inhibitor is useful for screening high degree
XX CC resistance xylanases for dough preparation. The xylanase is also useful
XX CC for preparing a non-sticky dough. A combination of xylanase and the
XX CC inhibitor is useful for calibrating and/or determining the quantity of
XX CC inhibitor in a wheat flour sample
XX XX
XX SQ Sequence 213 AA;

Query Match 99.1%; Score 1161; DB 3; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.3e-90; Indels 0; Gaps 0;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWTDGGGIYNAVNGSGGYSVNWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWTDGGGIYNAVNGSGGYSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKPTGSGNATITFSNHVNA 180

Qy 181 WKSHGMGLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMGLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 13
AA93753
ID AAY93753 standard; protein; 213 AA.
XX XX
XX AC AAY93753;
XX XX
XX DT 03-OCT-2000 (first entry)
XX XX
XX DE A bacterial endo-beta-1,4-xylanase mutant XM1.
XX XX
XX KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX KW dough; dough preparation.
XX OS Synthetic.
XX OS Bacillus subtilis.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 43 /note= "wild type Ile changed to Thr"
XX FT Misc-difference 197 /note= "wild type Met changed to Leu"
XX FT

KW Xylanase; Bacillus subtilis; baking; bread; yeast; food; foodstuffs;
XX bread; pastry.

OS Bacillus subtilis.

XX Key Location/Qualifiers
FH Peptide 1..28
FT /label= Signal peptide.

FT Misc-difference 7 /note= "Wild type amino acid substituted for Lys."

FT Misc-difference 13 /note= "Wild type amino acid substituted for Thr."

FT Misc-difference 16 /note= "Wild type amino acid substituted for Phe."

FT Misc-difference 21 /note= "Wild type amino acid substituted for Met."

FT Peptide 29..185

FT /label= Mature protein.

FT Misc-difference 30 /note= "Wild type amino acid substituted for Gly."

FT Misc-difference 43 /note= "Wild type amino acid substituted for Thr."

FT Misc-difference 150 /note= "Wild type amino acid substituted for Asn."

FT Misc-difference 171 /note= "Wild type amino acid substituted for Ala."

FT Misc-difference 197 /note= "Wild type amino acid substituted for Leu."

FT Misc-difference 203 /note= "Wild type amino acid substituted for Lys."

XX

PN DE4226528-A1.

XX

PD 17-FEB-1994.

XX 11-AUG-1992; 92DE-04226528.

PR 11-AUG-1992; 92DE-04226528.

XX (ROHG) ROEHM GMBH.

XX Gottschalk M, Sproesser B, Schuster E;

DR WPI; 1994-050809/08.

DR N-PSDB; AAQ56052.

XX New xylanase obtd. from Bacillus subtilis - useful in baking agents for

PT increased vol. of baking prods.

XX Claim 4; Page 10; lipp; German.

CC The modified xylanase is used as a baking agent, preferably for yeast

XX pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 213 AA;

Query Match 96.5%; Score 1130; DB 2; Length 213;
Best Local Similarity 95.3%; Pred. No. 5.6e-88;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MPKFKNPLVGLSALMSISLFSATASASTDYQWQNTDGGIVNAVNGSGGNYSVNWSN 60

Db 1 MPKFKKFLVGLTAAFMSISMFSAATASAGTDYQWQNTDGGITVNAVNGSGGNYSVNWSN 60

Qy 61 TGNFVVGKGTTPRINTYNAGVWAPNGGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120

Db 61 TGNFVVGKGTTPRINTYNAGVWAPNGGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSNATITFSNVNA 180

Db 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSNATITFSNVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

4

Db 181 WKSHGMNLGSNWAYQVWATEGYKSSGSSNVTW 213

Search completed: February 3, 2006, 09:15:43
Job time : 94 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:18:08 ; Search time 23 Seconds
(without alignment)
891.051 Million cell updates/sec

Title: US-10-626-583-5

Perfect score: 1171

Sequence: 1 MFPEKQFLVGLSLALMSIS.....YQVATEGYQSSGSSNTVTW 213

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	1 I40569	endo-1,4-beta-xyla
2	1168	99.7	213	1 S01734	endo-1,4-beta-xyla
3	1165	99.5	213	1 S48126	endo-1,4-beta-xyla
4	864.5	73.8	210	2 C33762	endo-1,4-beta-xyla
5	651.5	55.6	241	2 T37005	endo-1,4-beta-xyla
6	637	54.4	240	1 J50591	endo-1,4-beta-xyla
7	621	53.0	240	1 S47512	endo-1,4-beta-xyla
8	609.5	52.0	644	1 I40712	endo-1,4-beta-xyla
9	600	51.2	225	1 S57477	endo-1,4-beta-xyla
10	594	50.7	333	1 J50590	endo-1,4-beta-xyla
11	594	50.7	335	2 T50601	endo-1,4-beta-xyla
12	578	49.4	232	2 J37577	endo-1,4-beta-xyla
13	577	49.3	221	1 S57469	endo-1,4-beta-xyla
14	552	47.1	227	2 S43919	endo-1,4-beta-xyla
15	540	46.1	219	2 S71472	endo-1,4-beta-xyla
16	530	45.3	197	1 A44597	endo-1,4-beta-xyla
17	525	44.8	221	2 JC7307	endo-1,4-beta-xyla
18	523	44.7	190	1 A44595	endo-1,4-beta-xyla
19	515.5	44.0	241	2 S71473	endo-1,4-beta-xyla
20	513	43.8	190	1 A44593	endo-1,4-beta-xyla
21	506	43.2	190	1 A44594	endo-1,4-beta-xyla
22	505	43.1	223	2 S39883	endo-1,4-beta-xyla
23	503	43.0	222	2 S39154	endo-1,4-beta-xyla
24	480.5	41.0	354	1 S51779	endo-1,4-beta-xyla
25	469	40.1	661	1 S51773	endo-1,4-beta-xyla
26	461.5	39.4	228	1 WWESXP	endo-1,4-beta-xyla
27	436	37.2	656	1 S59631	endo-1,4-beta-xyla
28	420	35.9	261	1 S12745	endo-1,4-beta-xyla
29	409	34.9	511	1 JQ1935	endo-1,4-beta-xyla

30	405	34.6	229	2 S39155	xylanase 2 - fungu
31	388	33.1	954	1 S20907	endo-1,4-beta-xyla
32	382.5	32.7	211	1 JC1198	endo-1,4-beta-xyla
33	381	32.5	211	1 S48229	endo-1,4-beta-xyla
34	377	32.2	789	2 S58235	endo-1,4-beta-xyla
35	375	32.0	211	2 S49542	endo-1,4-beta-xyla
36	361	30.8	209	2 JC4909	endo-1,4-beta-xyla
37	349.5	29.8	781	2 S51592	XynB precursor - R
38	336.5	28.7	802	2 S46910	xylanase, beta(1,3
39	271.5	23.2	607	2 S24754	endo-1,4-beta-xyla
40	264.5	22.6	607	2 S49528	endoxylanase - rum
41	262	22.4	608	2 B53295	xylanase (EC 3.2.1
42	245	20.9	266	1 S48865	endo-1,4-beta-xyla
43	133	11.4	313	2 T04776	hypothetical prote
44	126	10.8	50	2 A61149	endo-1,4-beta-xyla
45	120	10.2	666	2 A42296	lysozyme 2 (EC 3.2

ALIGNMENTS

RESULT 1

I40569

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Bacillus subtilis

N:Alternate names: xylanase A

C:Species: Bacillus subtilis

C>Date: 12-Aug-1996 #sequence revision 02-Jul-1998 #text change 09-Jul-2004

C:Accession: I40569; S39157; S39158; A53635; F69735; S51711

R:Wolf, M.; Geczi, A.; Simon, O.; Borriass, R.

Microbiology 141, 281-290, 1995

A>Title: Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis:

A:Reference number: I40370; MUID:95219081; PMID:7704256

A:Accession: I40569

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF

A:Molecule type: DNA

A:Residues: 1-22,'P' 24-213 <WOL>

A:Cross-references: UNIPROT:P18429; UNIPARC:UPI00000863D0; EMBL:Z34519; NID:G2995396; P1

A:Experimental source: strain 168

R:Paice, M.G.; Bourbonnais, R.; Desrochers, M.; Jurasek, L.; Yaguchi, M.

Arch. Microbiol. 144, 201-206, 1986

A>Title: A xylanase gene from Bacillus subtilis: nucleotide sequence and comparison with

A:Reference number: S39157

A:Accession: S39157

A:Molecule type: DNA

A:Residues: 1-213 <PA11>

A:Cross-references: UNIPARC:UPI00000336C9; EMBL:M36648; NID:G143842; PIDN:AAA22897.1; P1

A:Experimental source: strain PAP115

A:Accession: S39158

A:Molecule type: protein

A:Residues: 29-58;60-73;75-76 <PA12>

A:Cross-references: UNIPARC:UPI000015759E; UNIPARC:UPI0000172962; UNIPARC:UPI0000172963

A:Experimental source: strain PAP115

R:Miao, S.; Ziser, L.; Aebersold, R.; Withers, S.G.

Biochemistry 33, 7027-7032, 1994

A>Title: Identification of glutamic acid 78 as the active site nucleophile in Bacillus

A:Reference number: A53635; MUID:94271752; PMID:7911679

A:Accession: A53635

A>Status: preliminary

A:Molecule type: protein

A:Residues: 97-107 <MIA>

A:Cross-references: UNIPARC:UPI00000172964

R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lardinois, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipar, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Banchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69735
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-213 <XUN>
A:Cross-references: UNIPARC:UPI00000336C9; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CA
A:Experimental source: strain 168
C:Genetics:
A:Gene: xynA
A:Map position: 175 degrees
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:106/Active site: Glu #status predicted
P:200/Active site: Glu #status predicted

Query Match 100.0%; Score 1171; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.4e-80;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60
Db 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120

Qy 121 TYKGTVKSDDGTYDIYITRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYITRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 2
S01734
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor [validated] - *Bacillus circulans*
N:Alternate names: xylanase A
C:Species: *Bacillus circulans*
C:Date: 07-Jun-1990 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S01734
R:Yang, R.C.A.; MacKenzie, C.R.; Narang, S.A.
Nucleic Acids Res. 16, 7187, 1988
A:Title: Nucleotide sequence of a *Bacillus circulans* xylanase gene.
A:Reference number: S01734; MUID:86303346; PMID:3405767
A:Accession: S01734
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-213 <YAN>
A:Cross-references: UNIPROT:P09850; UNIPARC:UPI0000034D1C; EMBL:X07723; NID:g39462; PIDN
A>Note: part of this sequence, including the amino end of the mature protein, was confir
R:Wakarchuk, W.W.; Campbell, R.L.; Sung, W.L.; Davoodi, J.; Yaguchi, M.
Protein Sci. 3, 467-475, 1994
A:Title: Mutational and crystallographic analyses of the active site residues of the Bac
A:Reference number: A53181; MUID:94290322; PMID:8019418
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213
R:Campbell, R.L.
submitted to the Brookhaven Protein Data Bank, June 1994
A:Reference number: A52866; PDB:1XNB
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213
C:Genetics:
A:Gene: xlnA

C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:97,108,140/Binding site: substrate (Tyr, Tyr, Arg) #status experimental
F:106,200/Active site: Glu #status experimental

Query Match 99.7%; Score 1168; DB 1; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.9e-80;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60
Db 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120

Qy 121 TYKGTVKSDDGTYDIYITRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYITRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 3
S48126
endo-1,4-beta-xylanase (EC 3.2.1.8) S precursor - *Bacillus* sp. (strain YA-14)
N:Alternate names: xylanase S
C:Species: *Bacillus* sp.
A:Variety: strain YA-14
C:Date: 14-Jul-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S48126
R:Ju-Hyun, Y.; Park, Y.S.; Yum, D.Y.; Kim, J.M.; Kong, I.S.; Bai, D.H.
J. Microbiol. Biotechnol. 3, 139-145, 1993
A:Title: Nucleotide sequence and analysis of a xylanase gene (xyns) from alkali-tolerant
A:Reference number: S48126
A:Accession: S48126
A:Molecule type: DNA
A:Residues: 1-213 <JUH>
A:Cross-references: UNIPROT:Q59256; UNIPARC:UPI0000060D47; EMBL:X59058; NID:g458800; PII
A:Experimental source: strain YA-14
C:Genetics:
A:Gene: xynS
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase S #status predicted <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:106,200/Active site: Glu #status predicted

Query Match 99.5%; Score 1165; DB 1; Length 213;
Best Local Similarity 99.1%; Pred. No. 6.6e-80;
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60
Db 1 MFKFKNPLVGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120

```
QY 121 TYKGVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213

RESULT 4
C3762
endo-1,4-beta-xylanhydrolase BH0899 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C83762
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: C83762
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-210 <STO>
A:Cross-references: UNIPROT:Q9KEP3; UNIPARC:UPI00000DCBD1; GB:AP001510; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0899
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 73.8%; Score 864.5; DB 2; Length 210;
Best Local Similarity 74.2%; Pred. No. 1.6e-57;
Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 1 MFKFKFLVGLSALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSN 60
DB 1 MFKFKFLVGLSALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSN 60

QY 61 TGNFVVGKWTGSPFRITNYNAGVWAPNGYLYLGYWTRSPLEIYYVDSWGYRPTG 120
DB 59 TGNFVVGKWTGSPFRITNYNAGVWAPNGYLYLGYWTRSPLEIYYVDSWGYRPTG 118

QY 121 TYKGVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSGNATITFSNHVNA 180
DB 119 THRGFVSDGGTYDIYTTTRYNAPSIDGTQ-TFQQYWSVRSKRPTGSGNATITFSNHVNA 177

QY 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213
DB 178 WRNAGMNLGSSWSYQVLATEGYQSSGSSNVTVW 210

RESULT 5
T37005
endo-1,4-beta-xylanase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37005
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, August 1999
A:Reference number: Z21618
A:Accession: T37005
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-241 <OLI>
A:Cross-references: UNIPROT:Q9RI72; UNIPARC:UPI00000DB349; EMBL:AL109949; PIDN:CAB52919.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: xinc; SCODEB:SCJ11.34c
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 55.6%; Score 651.5; DB 2; Length 241;
Best Local Similarity 58.4%; Pred. No. 1.3e-41;
Matches 129; Conservative 25; Mismatches 50; Indels 17; Gaps 6;
```

```
QY 5 KKNFLVG---LSAALMSISLFSATASAAST-----DYQWNTDGGGIVNAVNGSG 51
DB 23 RRGFLGGAGTALATASGLLLPGTAHAATTTTQTGDTGMYTSPFTDGGGVSMTLNGG 82

QY 52 GNYSVNSNTGNFVVGKWTGSPFRITNYNAGVWAPNGYLYLGYWTRSPLEIYYVVD 111
DB 83 GSYSQTWNTNCGNFVAGKGMSTGGR-RTVRYN-GYFNPNGYGLYGTWISNPLVEIYVD 140

QY 112 SWGTYRPTGYTKGVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSGNAT 171
DB 141 NMGYSRPTGYTKGVKSDGGTYDIYTTTRYNAPSVEGK-TFQQYWSVRSKRPTGSGS-GT 198

QY 172 ITFSNHVNAWKSHGMNLGNSWAYQVMATEGYQSSGSSNVTV 212
DB 199 ITTGNHFDARAGNMGQFRYIMATEGYQSSGSSNITV 239

RESULT 6
J50591
endo-1,4-beta-xylanase (EC 3.2.1.8) C precursor - Streptomyces lividans
N:Alternate names: xylanase C
C:Species: Streptomyces lividans
C:Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: J50591; PS0240
R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A:Reference number: J50589; MUID:92077439; PMID:1743521
A:Accession: J50591
A:Molecule type: DNA
A:Residues: 1-240 <SHA>
A:Cross-references: UNIPROT:P26220; UNIPARC:UPI0000034D31; GB:M64553; NID:g153530; PIDN
A:Accession: PS0240
A:Molecule type: protein
A:Residues: 50-80 <SH2>
A:Cross-references: UNIPARC:UPI0000172965
C:Genetics:
A:Gene: xinc
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-49/Domain: signal sequence #status predicted <SIG>
F:50-240/Product: endo-1,4-beta-xylanase C #status experimental <MAT>
F:62-239/Domain: endo-1,4-beta-xylanase homology <XYL>
F:134,226/Active site: Glu #status predicted

Query Match 54.4%; Score 637; DB 1; Length 240;
Best Local Similarity 57.5%; Pred. No. 1.6e-40;
Matches 127; Conservative 24; Mismatches 52; Indels 18; Gaps 6;

QY 5 KKNFLVG---LSAALMSISLFSATASAAST-----DYQWNTDGGGIVNAVNGSG 51
DB 23 RRGFLGGAGTALATASGLLLPGTAHAATTTTQTGDTGMYTSPFTDGGGVSMTLNGG 82

QY 52 GNYSVNSNTGNFVVGKWTGSPFRITNYNAGVWAPNGYLYLGYWTRSPLEIYYVVD 111
DB 83 GSYSQTWNTNCGNFVAGKGMSTGD-GNVRYN-GYFNPNGYGLYGTWISNPLVEIYVD 139

QY 112 SWGTYRPTGYTKGVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSGNAT 171
DB 140 NMGYSRPTGYTKGVKSDGGTYDIYTTTRYNAPSVEGK-TFQQYWSVRSKRPTGSGS-GT 197

QY 172 ITFSNHVNAWKSHGMNLGNSWAYQVMATEGYQSSGSSNVTV 212
DB 198 ITTGNHFDARAGNMGQFRYIMATEGYQSSGSSNITV 238

RESULT 7
S47512
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - Streptomyces sp.
N:Alternate names: xylanase
```

Best Local Similarity 57.4%; Pred. No. 5.1e-38;
Matches 124; Conservative 29; Mismatches 44; Indels 19; Gaps 7;

QY 9 LVGLSA--ALMSISLFSATASAASTD-----YWQNWTGGGIVNAVNGSGGNYSV 56
| | | :
Db 20 LTCLLAGALVAGALAAPAAAAVTNTTGTHDGYFYSFWTDSPGSVSMDLNSGGCYT- 78
| | | :
QY 57 NWSNTGNFVVGGKWTGTSPRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDMSGTY 116
| | | :
Db 79 RWSNTGNFVAGKWSGTGR-KTVSY-SGQPNPSRNAYLTLYGWTSPLVEYIYVDSMGTY 136
| | | :
QY 117 RPTGYTKGVKSDGGTYDIYTTRYNAPSIDGDRITFTQWSVRQSQRKPTGSNATIIFSN 176
| | | :
Db 137 RPTGTFMGTSDGGTYDIYRTORVNKPSTEGSDSTFYQYSVRQQKRGTG---TITSGN 193
| | | :
QY 177 HVNAWKSHGMNLGSNWAYOVMATGYQGSSSNVTW 212
| | | :
Db 194 HFDWAWSKGNLGRH-NYMIMATEGYQSSGSSITV 228
| | | :

RESULT 9
S57477
endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Emericella nidulans
N;Alternate names: xylanase 1
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: S57477
R;Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A;Description: Expression in Saccharomyces cerevisiae of two xylanase encoding
A;Reference number: S57469
A;Accession: S57477
A;Molecule type: DNA
A;Residues: 1-225 <PER>
A;Cross-references: UNIPROT:P55332; UNIPARC:UPI0000139073; EMBL:Z49892; NID:g87
C;Genetics:
A;Introns: 93/2
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylns
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F;48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F;121,212/Active site: Glu #status predicted

Query Match 51.2%; Score 600; DB 1; Length 225;
Best Local Similarity 56.8%; Pred. No. 8.4e-38;
Matches 121; Conservative 29; Mismatches 41; Indels 22; Gaps 8;

QY 9 LVGLSALMSISLFSATASASTDYQN-----WTDGGGIVNAVNGSGGNYSVWNSNTG 62
| | | :
Db 27 LAAREASLLSRTPSGTG-----NSNGYYYSFWDGGDVITYTGAGSGSYTQWNSVG 79
| | | :
QY 63 NFVVGKGWTTGSPRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDMSGTYRP--TG 120
| | | :
Db 80 NFVVGKGWNPST-RIIINY-GGSFNPSGNCYLAVYGTQNPFLIEYIVESVGTVPNGSGG 137
| | | :
QY 121 TYFGTVKSDGGTYDIYTTRYNAPSIDGDRITFTQWSVRQSQRKPTGSNATIIFSNHVA 180
| | | :
Db 138 QHRGTVYSDGATYDIYATRYNAPSIEG-TATPEQFWSVRQSQRKTG---TVTIANHFNA 193
| | | :
QY 181 WKSHGMNLGSNWAYOVMATGYQGSSSNVTW 213
| | | :
Db 194 WAALGMRLGTH-NYQIVATEGYQSSGSSITV 225
| | | :

RESULT 10
JS0590
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
N;Alternate names: xylanase B
C;Species: Streptomyces lividans

C>Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
C:Accession: JS0590; PS0239
R:Shareck, E.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A:Reference number: JS0589; MUID:92077439; PMID:1743521
A:Accession: JS0590
A:Molecule type: DNA
A:Residues: 1-333 <SHA>
A:CROSS-references: UNIPARC:UPI000017296A; GB:M64552
A:Accession: PS0239
A:Molecule type: protein
A:Residues: 41-71 <SH2>
A:CROSS-references: UNIPARC:UPI000017296B
C:Genetics:
A:Gene: xlnB
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-40/Domain: signal sequence #status predicted <SIG>
F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
F:54-230/Domain: endo-1,4-beta-xylanase homology <XYL>
F:127,217/Active site: Glu #status predicted

Query Match 50.7%; Score 594; DB 1; Length 333;
Best Local Similarity 62.2%; Pred. No. 3.6e-37;
Matches 112; Conservative 19; Mismatches 43; Indels 6; Gaps 4;

QY 33 YWQNTDGGGIVNAVNGSGNYVNMSTGNFVVGKGTGSPPTTINYNAGVWAPNGNG 92
DB 56 YYSFWTDSQGTVMNMGSGGYSTSWRNTGNFVAGKWANGR-RTVQY-SGSFNPSSGNA 113

QY 93 YLTLYGWTRSPLIEYYVVDVSMGTGTYKGTGKTSKDGTDYITTTTRYNAPSIDGDRTT 152
DB 114 YLALYGTSTNPLVEYYIVDNGTGYPTGEYKGTVTSDGTYDIYKTRVKNKPSVETR-T 172

QY 153 FTQYMSVRSQKRPSTGSNATITFSNHVNAWKSHGMNLGNWAYQVNMATGYSQSSGSSNVTV 212
DB 173 FDQYMSVRSQKRTG---TITGNHFDARAGMPLGNFYSYMIATGYSQSSGTSIN 229

RESULT 11
T50601
endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor
N:Alternate names: xylanase B
C:Species: Streptomyces coelicolor
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50601
R:Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996
A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S
A:Reference number: Z20556; MUID:97000351; PMID:8843436
A:Accession: T50601
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <RED>
A:CROSS-references: UNIPROT:Q9RKN6; UNIPARC:UPI00000DC56E; EMBL:AL133220; PIDN:CAB61738.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: xlnB
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase

Query Match 50.7%; Score 594; DB 2; Length 335;
Best Local Similarity 62.2%; Pred. No. 3.6e-37;
Matches 112; Conservative 19; Mismatches 43; Indels 6; Gaps 4;

QY 33 YWQNTDGGGIVNAVNGSGNYVNMSTGNFVVGKGTGSPPTTINYNAGVWAPNGNG 92
DB 57 YYSFWTDSQGTVMNMGSGGYSTSWRNTGNFVAGKWANGR-RTVQY-SGSFNPSSGNA 114

QY 93 YLTLYGWTRSPLIEYYVVDVSMGTGTYKGTGKTSKDGTDYITTTTRYNAPSIDGDRTT 152
DB 115 YLALYGTSTNPLVEYYIVDNGTGYPTGEYKGTVTSDGTYDIYKTRVKNKPSVETR-T 173

QY 153 FTQYMSVRSQKRPSTGSNATITFSNHVNAWKSHGMNLGNWAYQVNMATGYSQSSGSSNVTV 212
DB 174 FDQYMSVRSQKRTG---TITGNHFDARAGMPLGNFYSYMIATGYSQSSGSSINV 230

RESULT 12
JC7577
endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
N:Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
C:Species: Aspergillus oryzae
C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7577; PC7120
R:Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000
A:Title: Molecular cloning, overexpression, and purification of a major xylanase from A:
A:Reference number: JC7577; MUID: 21077500; PMID:11210150
A:Accession: JC7577
A:Molecule type: DNA
A:Residues: 1-232 <KIM>
A:CROSS-references: UNIPROT:Q9HFA4; UNIPARC:UPI0000069976; DBU:AB044941
A:Experimental source: strain KEN616
A:Accession: PC7120
A:Molecule type: protein
A:Residues: 45-64 <K12>
A:CROSS-references: UNIPARC:UPI0000175A84
C:Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, d:
C:Genetics:
A:Gene: xynG2
A:Introns: 100/2
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase

Query Match 49.4%; Score 578; DB 2; Length 232;
Best Local Similarity 52.1%; Pred. No. 3.8e-36;
Matches 122; Conservative 31; Mismatches 47; Indels 34; Gaps 9;

QY 7 NFLVGLSAAALMSIS-----LFSATA-----SAASTD-----YQWNWDGG 41
DB 6 SILLACSAAGALATPIEPLADHPNEAFNEAFNDLVGRSTPSTGYNNGYYSFTWDGG 65

QY 42 GIVNAVNGSGNYVNMSTGNFVVGKGTGSPPTTINYNAGVWAPNGNGYLYGWTR 101
DB 66 GDVITYTNGSGSYVQSNVGNFVGGKGNPSS-RAITY-SGSFNPSSGNYLAVYGT 123

QY 102 SPLIEYYVVDVSMGTGTYKGTGKTSKDGTDYITTTTRYNAPSIDGDRTTFTQYMSV 159
DB 124 DPLIEYYIVESYGTYNPGSGTYKGTGTSDDGTYNITSVRTNAPSIIIG-TATFTQYMSV 182

QY 160 ROSKRPSTGSNATITFSNHVNAWKSHGMNLGNWAYQVNMATGYSQSSGSSNVTVW 213
DB 183 RTSKRVGG---TVTGNHFNWAKYGLTLGTH-NYQIVATEGYSQSSSAITVY 232

RESULT 13
S57469
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans
N:Alternate names: xylanase 2
C:Species: Emericella nidulans, Aspergillus nidulans
C>Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S57469
R:Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A:Description: Expression in Saccharomyces cerevisiae of two xylanase encoding genes fr:
A:Reference number: S57469
A:Accession: S57469
A:Molecule type: DNA
A:Residues: 1-221 <PER>
A:CROSS-references: UNIPROT:P55333; UNIPARC:UPI0000139075; EMBL:Z49893; NID:g870834; PFI:
C:Genetics:

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:15:58 ; Search time 108 Seconds
(without alignment)
1391.459 Million cell updates/sec

Title: US-10-626-583-5
Perfect score: 1171
Sequence: 1 MFPEKKPLVGLSALMSIS.....YQVMATEGYQSSGSNTVTV 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	1 Xyna_BACSU	P18429 bacillus su
2	1168	99.7	213	1 Xyna_BACCI	P09850 bacillus ci
3	1166	99.6	213	2 Q59254 BACSU	Q59254 bacillus su
4	1165	99.5	213	2 Q59256 9BACI	Q59256 bacillus sp
5	1150	98.2	213	2 Q8RMN9 BACSU	Q8RMN9 bacillus su
6	1144	97.7	213	2 Q8RMN8 BACCI	Q8RMN8 bacillus ci
7	1127	96.2	213	2 Q82B36 BACSP	Q82B36 bacillus sp
8	1104	94.3	213	2 Q84F19 9BACI	Q84F19 bacillus sp
9	1096	93.6	213	2 Q8VVC3 9BACI	Q8VVC3 bacillus sp
10	945.5	80.7	212	2 Q9F9B9 9BACL	Q9F9B9 paenibacill
11	935.5	79.9	214	2 Q6TLP3 9BACT	Q6TLP3 uncultured
12	930	79.4	210	1 Xyna_BACST	P45705 bacillus st
13	929	79.3	211	2 Q43993 AERPU	Q43993 aeromonas p
14	864.5	73.8	210	2 Q71S35 BACFI	Q71S35 bacillus fi
15	864.5	73.8	210	2 Q9KEF3 BACHD	Q9KEF3 bacillus ha
16	863.5	73.7	210	2 Q8U894 BACFI	Q8U894 bacillus fi
17	663.5	56.7	335	2 Q8RQ88 9MICO	Q8RQ88 xylanimicro
18	659	56.3	338	2 Q56285 THEFU	Q56285 thermomonos
19	659	56.3	338	2 Q8Z998 THEFU	Q8Z998 thermomonos
20	651.5	55.6	241	2 Q9R172 STRCO	Q9R172 streptomyce
21	646	55.2	329	2 Q9RMH9 STRVD	Q9RMH9 streptomyce
22	645.5	55.1	335	2 Q8RMW4 STRTM	Q8RMW4 streptomyce
23	639.5	54.6	335	2 Q76BV2 STRTL	Q76BV2 streptomyce
24	637	54.4	240	1 XINC_STRLI	P28220 streptomyce
25	630	53.8	344	2 Q8GMV7 9ACTO	Q8GMV7 nonomuraea
26	626	53.5	191	2 Q9EW89 STROI	Q9EW89 streptomyce
27	622	53.1	228	2 Q59962 9ACTO	Q59962 streptomyce
28	621.5	53.1	228	2 Q4WG11 ASPFU	Q4WG11 aspergillus
29	621	53.0	240	2 Q56013 9ACTO	Q56013 streptomyce
30	610.5	52.1	417	2 Q593B5 9ALTE	Q593B5 microbulbif
31	609.5	52.0	644	1 XYNB_CELFI	P54865 cellulomona

RESULT 1
Xyna_BACSU
ID Xyna_BACSU

STANDARD; PRT; 213 AA.

AC P18429;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-

DE beta-D-xylan xylanohydrolase A).

GN Name=xyna; OrderedLocusNames=BSU18840;

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RP NUCLEOTIDE SEQUENCE.

RT Palce M.G., Bourbonnais R., Desrochers M., Jurassek L., Yaguchi M.;

RT "A xylanase gene from Bacillus subtilis: nucleotide sequence and

RT comparison with B. pumilus gene.";

RL Arch. Microbiol. 144:201-206(1986).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;

RA "Sequence analysis of the Bacillus subtilis chromosome region between

RA the terC and chrAB loci cloned in a yeast artificial chromosome.";

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=168;

RA Kunitz F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Chai S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.-Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,

RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,

RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,

RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,

RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,

RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,

RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,

RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,

RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,

RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,

RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,

RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,

RA Scoffone F., Sekiguchi J., Sekowska A., Setor S.J., Serro P.,

RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,

RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P.,

RA Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vannier F.,

ALIGNMENTS

```

RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yaumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
RN [4]
RN MUTAGENESIS.
RP Wakarchuk W., Methot N., Lanthier P., Sung W., Seligy V., Yaguchi M.,
RA To R., Campbell R., Rose D.;
RL (in) Visser J., Beldman G., Kusters-van Someren M.A., Voragen A.G.J.
RL (eds.);
RL Xylans and xylanases, pp.439-442, Elsevier, Amsterdam (1992).
RN [5]
RN ACTIVE SITE GLU-106.
RX MEDLINE=94271752; PubMed=7911679;
RA Miao S., Ziser L., Rebersold R., Withers S.G.;
RT "Identification of glutamic acid 78 as the active site nucleophile in
RT Bacillus subtilis xylanase using electrospray tandem mass
RT spectrometry.";
RL Biochemistry 33:7027-7032(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M36648; AAA22897.1; -; Genomic DNA.
CC EMBL; AF027868; AAB84458.1; -; Genomic DNA.
CC EMBL; Z99114; CAB13776.1; -; Genomic DNA.
DR PIR; I40569; I40569.
DR SDB; IAXK; X-ray; A/B=-.
DR PMR; P18429; 27-213.
DR Subtilist; BG10808; xyna.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR 3D-structure; Complete proteome; Glycosidase; Hydrolase; Signal;
KW Xylan degradation..
FT SIGNAL 1 28
FT CHAIN 29 213
FT ACT_SITE 106 106
FT MUTAGEN E->S: Drastically reduced activity.
FT MUTAGEN E->S: Drastically reduced activity.
SQ SEQUENCE 213 AA; 23345 MW; 20CBA5238CC0564 CRC64;

Query Match
Best Local Similarity 100.0%; Score 1171; DB 1; Length 213;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFKKFLVLGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGGNYVNWNS 60
Db 1 MPFKKFLVLGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGGNYVNWNS 60
QY 61 TGNFVVGKWTGSPFRINTYNAGVWPNNGYLTLGWTRSPLEYYVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRINTYNAGVWPNNGYLTLGWTRSPLEYYVDSWGTYRPTG 120
QY 121 TYKGVKSDGGTYDYITTYTRNAPSIDGDRITFTQYWSVRQSKRPTGNSNATIFSNHYNA 180
Db 121 TYKGVKSDGGTYDYITTYTRNAPSIDGDRITFTQYWSVRQSKRPTGNSNATIFSNHYNA 180
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213

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Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
|||||
RESULT 2
XNA_BACCI STANDARD; PRT; 213 AA.
ID XNA_BACCI STANDARD; PRT; 213 AA.
AC P09850;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN Name=xlnA;
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88303346; PubMed=3405767;
RA Yang R.C.A., Mackenzie C.R., Narang S.A.;
RT "Nucleotide sequence of a Bacillus circulans xylanase gene.";
RL Nucleic Acids Res. 16:7187-7187(1988).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND MUTAGENESIS.
RX MEDLINE=94290322; PubMed=8019418;
RA Wakarchuk W.W., Campbell R.L., Sung W.L., Davoodi J., Yaguchi M.;
RT "Mutational and crystallographic analyses of the active site residues
RT of the Bacillus circulans xylanase.";
RL Protein Sci. 3:467-475(1994).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=96322313; PubMed=8756457; DOI=10.1021/bi9613234;
RA McIntosh L.P., Hand G., Johnson P.E., Joshi M.D., Koerner M.,
RA Plesniak L.A., Ziser L., Wakarchuk W.W., Withers S.G.;
RT "The pKa of the general acid/base carboxyl group of a glycosidase
RT cycles during catalysis: a 13C-NMR study of Bacillus circulans
RT xylanase.";
RL Biochemistry 35:9958-9966(1996).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X07723; CAA30553.1; -; Genomic DNA.
DR PIR; S01734; S01734.
DR PDB; 1BCX; X-ray; @=29-213.
DR PDB; 1BVV; X-ray; @=29-213.
DR PDB; 1C5H; X-ray; A=29-213.
DR PDB; 1C5I; X-ray; A=29-213.
DR PDB; 1HV0; X-ray; A=29-213.
DR PDB; 1HV1; X-ray; A=29-213.
DR PDB; 1XNB; X-ray; @=29-213.
DR PDB; 1XNC; X-ray; @=29-213.
DR PDB; 2BVV; X-ray; A=29-213.
DR InterPro; IPR001137; Glyco_hydro_11; 1.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR 3D-structure; Glycosidase; Hydrolase; Signal; Xylan degradation.
KW SIGNAL 1 28
FT CHAIN 29 213
FT ACT_SITE 106 106
FT ACT_SITE 200 200
FT STRAND 200 33
FT Endo-1,4-beta-xylanase.
FT Nucleophile.
FT Proton donor.

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FT STRAND 43 48
FT TURN 51 52
FT STRAND 53 59
FT STRAND 63 70
FT TURN 75 76
FT STRAND 78 89
FT STRAND 92 101
FT TURN 102 104
FT STRAND 105 113
FT STRAND 121 128
FT TURN 129 130
FT STRAND 131 144
FT TURN 146 147
FT STRAND 150 160
FT STRAND 170 173
FT HELIX 174 183
FT TURN 184 185
FT STRAND 191 202
FT STRAND 205 213
SQ SEQUENCE 213 AA; 23359 MW; 4BA0A35238CC0135 CRC64;

Query Match 99.7%; Score 1168; DB 1; Length 213;
Beat Local Similarity 99.5%; Pred. No. 4e-86;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFKFKNFVLGLSAAALMSISLFSATASAASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60
DB 1 MFKFKNFVLGLSAAALMSISLFSATASAASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGLYLTGWTSPLEIYYVDSWGTYRPTG 120
DB 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGLYLTGWTSPLEIYYVDSWGTYRPTG 120

QY 121 TYKGTVKSDDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
DB 121 TYKGTVKSDDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180

QY 181 WKSHGMNLGSWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSWAYQVMATEGYQSSGSSNVTVW 213

RESULT 3
Q59254 BACSU PRELIMINARY; PRT; 213 AA.
AC Q59254;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Xylanase (EC 3.2.1.8).
GN Name=xynA;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168 trpC2;
RX MEDLINE=92140374; PubMed=1310524;
RA Nierebach M., Kreuzaler P., Geerse R.H., Postma P.W., Hirsch H.J.;
RT "Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA
gene, encoding PEP synthase.";
RL Mol. Gen. Genet. 231:332-336(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168 trpC2;
RX MEDLINE=95219081; PubMed=7704256;
RA Wolf M., Geczi A., Simon O., Borriass R.;
RT "Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus
subtilis: characterization, mapping and construction of strains
deficient in lichenase, cellulase and xylanase.";
RL Microbiology 141:281-290(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
```

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RC STRAIN=168 trpC2;
RA Borriass R., Wolf M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z34519; CAA84276.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q59254; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 213 AA; 23355 MW; 21D76D4F8CED4B7 CRC64;

Query Match 99.6%; Score 1166; DB 2; Length 213;
Beat Local Similarity 99.5%; Pred. No. 5.8e-86;
Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFKFKNFVLGLSAAALMSISLFSATASAASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60
DB 1 MFKFKNFVLGLSAAALMSISLFSATASAASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGLYLTGWTSPLEIYYVDSWGTYRPTG 120
DB 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGLYLTGWTSPLEIYYVDSWGTYRPTG 120

QY 121 TYKGTVKSDDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
DB 121 TYKGTVKSDDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180

QY 181 WKSHGMNLGSWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSWAYQVMATEGYQSSGSSNVTVW 213

RESULT 4
Q59256 9BACI PRELIMINARY; PRT; 213 AA.
AC Q59256;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
GN Name=xynS;
OS Bacillus sp. YA-14.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=72411;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YA-14;
RA Yu J.H., Park Y.S., Yum D.Y., Kim J.M., Kong I.S., Bai D.H.;
RT "Nucleotide sequence and analysis of a xylanase gene (xynS) from
alkali-tolerant Bacillus sp. YA-14 and comparison with other
xylanases.";
RL J. Microbiol. Biotechnol. 3:139-145(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YA-14;
RA Hyun Ju Y.;
RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X59058; CAA41783.1; -; Genomic_DNA.
DR PIR; S48126; S48126.
DR HSSP; P09850; 1XNB.
DR SMR; Q59256; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
```

DR PROSITE; PS00776; GLYCOSYL HYDROL F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL HYDROL F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 213 endo-1, 4-beta-xylanase.
SQ SEQUENCE 213 AA; 23341 MW; 2110D35768CC0034 CRC64;

Query Match 99.5%; Score 1165; DB 2; Length 213;
Best Local Similarity 99.1%; Pred. No. 7e-86;
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAALMSISLFSATASASTDYQNWTDDGGIYNVAVNGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLSAALMSISLFSATASASTDYQNWTDDGGIYNVAVNGSGNYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120

Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRSKRPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWVATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWVATEGYQSSGSSNVTVM 213

RESULT 5
Q8RMN9_BACSU PRELIMINARY; PRT; 213 AA.
AC Q8RMN9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1,4-xylanase.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun J., Gu S., Li W., Xu Z., Zhao H., Xiao J., Fu L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490979; AAM08359.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN9; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL HYDROL F11_1; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23277 MW; 34DFAD4D9C2C0034 CRC64;

Query Match 98.2%; Score 1150; DB 2; Length 213;
Best Local Similarity 98.6%; Pred. No. 1.1e-84;
Matches 210; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAALMSISLFSATASASTDYQNWTDDGGIYNVAVNGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLSAALMSISLFSATASASTDYQNWTDDGGIYNVAVNGSGNYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120

Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRSKRPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWVATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWVATEGYQSSGSSNVTVM 213

RESULT 6
Q8RMN8_BACCI PRELIMINARY; PRT; 213 AA.
AC Q8RMN8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1,4-xylanase.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun J., Xu Z., Li W., Gu S., Zhao H., Xiao J., Chen Y.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490980; AAM08360.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN8; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL HYDROL F11_1; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23378 MW; E306B98D49E8CF4D CRC64;

Query Match 97.7%; Score 1144; DB 2; Length 213;
Best Local Similarity 97.7%; Pred. No. 3.4e-84;
Matches 208; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAALMSISLFSATASASTDYQNWTDDGGIYNVAVNGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLSAALMSISLFSATASASTDYQNWTDDGGIYNVAVNGSGNYSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTG 120

Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRSKRPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWVATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWVATEGYQSSGSSNVTVM 213

RESULT 7
Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.
AC Q9ZB36;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanhydrolase.
GN Name=xynA;
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim S.C., Jeong K.J., Kim M.S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U51675; AAD10834.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q9ZB36; 27-213.

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DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Hydrolase.
SQ SEQUENCE 213 AA; 23277 MW; 3A1DEE1139E3358B CRC64;

Query Match 96.2%; Score 1127; DB 2; Length 213;
Best Local Similarity 94.8%; Pred. No. 8e-83;
Matches 202; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFKFKNLFVLGLTAALMSISLFSATASASTDYQWQNTDGGGVNVAVNGSGGNYSVNWSN 60
DB 1 MFKFKNLFVLGLTAALMSISLFSATASASTDYQWQNTDGGGVNVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
DB 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 8
Q84F19_9BACI PRELIMINARY; PRT; 213 AA.
AC Q84F19;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor.
GN Name=xynA;
OS Bacillus sp. BP-7.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=126733;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15057452; DOI=10.1007/s00284-003-4196-0;
RA Gallardo O., Diaz P., Pastor F.I.J.;
RT "Cloning and characterization of xylanase A from the strain Bacillus
sp. BP-7: comparison with alkaline pi-low molecular weight xylanases
of family 11.";
RL Curr. Microbiol. 48:276-279(2004).
DR EMBL; AJ536759; CAD60654.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q84F19; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal; Xylan degradation.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 213 endo-1,4-beta-xylanase A.
FT SEQUENCE 213 AA; 23475 MW; F1E194D24A329516 CRC64;

Query Match 94.3%; Score 1104; DB 2; Length 213;
Best Local Similarity 93.0%; Pred. No. 5.7e-81;
Matches 198; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MFKFKNLFVLGLTAALMSISLFSATASASTDYQWQNTDGGGVNVAVNGSGGNYSVNWSN 60
DB 1 MFKFKNLFVLGLTAALMSISLFSATASASTDYQWQNTDGGGVNVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
DB 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 9
Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.
AC Q8VVC3;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Endo-xylanase.
GN Name=xylS;
OS Bacillus sp. NBL420.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=165829;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hong I.P., Lee S.Y., Choi S.G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF441773; AAL32473.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8VVC3; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23341 MW; 4CC0DFF525E7551 CRC64;

Query Match 93.6%; Score 1096; DB 2; Length 213;
Best Local Similarity 92.5%; Pred. No. 2.5e-80;
Matches 197; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 MFKFKNLFVLGLTAALMSISLFSATASASTDYQWQNTDGGGVNVAVNGSGGNYSVNWSN 60
DB 1 MFKFKNLFVLGLTAALMSISLFSATASASTDYQWQNTDGGGVNVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
DB 61 TGNFVVGKWTGSPFRITNNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 10
Q9F9B9_9BACL PRELIMINARY; PRT; 212 AA.
AC Q9F9B9;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
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DE Xylanase A.
OS Paenibacillus sp. KCTC8848P.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
NCBI_TaxID=109199;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KCTC 8848P.
RA Lee H.J., Shin D.J., Cho N.C., Im S.Y., Lee H.B., Chun S.B., Bai S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF195421; AAG33526.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q9F8B9; 25-212.
DR GO; GO:0004533; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation.
SQ SEQUENCE 212 AA; 23258 MW; 1A1ABC825BED93D2 CRC64;

Query Match 80.7%; Score 945.5; DB 2; Length 212;
Best Local Similarity 79.3%; Pred. No. 3.2e-68;
Matches 169; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSGGYSVNMNSN 60
Db 1 MFKSSKLLTVLAAASMSFGPFASSTNAA-TDYQWNTDGGGTVNAVNGSGGYSVTWKN 59

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLWGTRSPLEIYYVVDVDSWGTYRPTG 120
Db 60 SGNFVVGKWTGSPDRITINYNAGVWAPSGNGYLYLWGTRNSLIYYVVDVDSWGTYRPTG 119

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGNSNATITFSNHVN 180
Db 120 TYKGTVTS DGGTYDIYTTMRVDAPSIEGQRTFTQYWSVRQKRPITGNTITFSNHVKA 179

Qy 181 WKSHGMNLSNWAYQVNMATEGYQSSGSSNVTW 213
Db 180 WARQGMHLGNWSVQLATEGYQSSGSSNVTW 212

RESULT 11
ID Q6TLP3_9BACT PRELIMINARY; PRT; 214 AA.
AC Q6TLP3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed14718652; DOI=10.1110/ps.03333504;
RA Palackal N., Brennan Y., Callen W.N., Dupree P., Frey G., Goubet F.,
RA Hazlewood G.P., Healey S., Kang Y.E., Kretz K.A., Lee E., Tan X.,
RA Tomlinson G.L., Verruto J., Wong V.W.K., Mathur E.J., Short J.M.,
RA Robertson D.E., Steer B.A.;
RT "An evolutionary route to xylanase process fitness.";
RL Protein Sci. 13:494-503(2004).
DR EMBL; AY394562; AAQ90180.2; -; Genomic_DNA.
DR HSSP; P09850; 1BCX.
DR SMR; Q6TLP3; 30-214.
DR GO; GO:0031176; P:carbohydrate metabolism; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
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DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 29 Potential.
SQ SEQUENCE 214 AA; 23478 MW; 6FD1CB9BB66A5048 CRC64;

Query Match 79.9%; Score 935.5; DB 2; Length 214;
Best Local Similarity 80.4%; Pred. No. 2.1e-67;
Matches 172; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSGGYSVNMNSN 59
Db 1 MFKSSKLLTVLAAASMSFISLFTVTAASSTDYQWNTDGGGTVNAVNGSGGYSVMS 60

Qy 60 NTGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYLWGTRSPLEIYYVVDVDSWGTYRPT 119
Db 61 NCGNFVVGKWTGTSATRVINYNAGAFSPSGNGYLYLWGTRNSLIYYVVDVDSWGTYRPT 120

Qy 120 GTYKGTVKS DGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGNSNATITFSNHVN 179
Db 121 GTYKGTVTS DGGTYDIYTTTRTNAPSIDGNNTTFTQFWSVRQSKRPITGNTTITFSNHVN 180

Qy 180 AWKSHGMNLSNWAYQVNMATEGYQSSGSSNVTW 213
Db 181 AWKSKGMNLSNWSVQLATEGYQSSGYSNVTW 214

RESULT 12
XNA_BACST
ID XNA_BACST STANDARD; PRT; 210 AA.
AC P45705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-
DE beta-D-xylan xylanohydrolase A).
DE Name=xynA;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=No. 236;
RA Cho S., Choi Y.;
RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
RT Bacillus stearothermophilus.";
RL J. Microbiol. Biotechnol. 5:117-124(1995).
RN [2]
RP SEQUENCE REVISION.
RA Cho S., Choi Y.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -! PATHWAY: Xylan degradation.
CC -! SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U15985; AAB72117.1; -; Genomic_DNA.
CC HSSP; P09850; 1XNB.
CC SMR; P45705; 24-210.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PR00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 19 Potential.
```

FT	CHAIN	20	210	Endo-1,4-beta-xylanase A.
FT	ACT_SITE	104	104	Nucleophile (By similarity).
FT	ACT_SITE	197	197	Proton donor (By similarity).
SO	SEQUENCE	210 AA;	23221 MW;	3190CF74C34AAB45 CRC64;
	Query Match	79.4%;	Score 930;	DB 1; Length 210;
	Best Local Similarity	80.6%;	Pred No. 5,6e-67;	
	Matches 170;	Conservative 11;	Mismatches 26;	Indels 2; Gaps 2;
Qy	3	KFKXNFLVGLSAAALMSISLFSATASAASTDYQWNWDGGGIYNAVNGSGGNYSVNWSNTG	62	
Db	2	KLKKKMLTLTLTASMSFGLGATSAATDYYQYWTDDGGGMVNAVNGPGNYSVTWQNTG	60	
Qy	63	NFVVGKGGTTGSPERTINYNAGVAPNGVYLTLYGWTSPLEIYYVVDNSGTYRPTGTY	122	
Db	61	NFVVGKGGTTGSPNRKVINYNAGIWEPSNGVYLTLYGWTNRNALIEYYVVDNSGTYRPTGNY	120	
Qy	123	KGTVKSDDGTYDIIYTTTTRYNAPSIDGDRITTFQYMSVRSQSKRPTGSNATITFSNHVNNAWK	182	
Db	121	KGTVNSDDGTYDIIYTTTRYNAPSIDGTQ-TTQQFWSVRSQSKRPTGSNVIITFSNHVNAWR	179	
Qy	183	SHGMNLGNSWAYQVWATEGYOSSSSNVTWV	213	
Db	180	SKGMNLGNSWAYQVLTATEGYOSSGRSNVTWV	210	
RESULT 13				
QD	Q43993_AERPU	PRELIMINARY;	PRT;	211 AA.
AC	Q43993;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Xylanase I precursor.			
GN	Name=xyna;			
OS	Aeromonas punctata (Aeromonas caviae).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;			
OC	Aeromonadaceae; Aeromonas.			
OX	NCBI_TaxID=648;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=ME-1; TISSUE=Gut content of silk worm;			
RA	Kubata K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.;			
RT	"Xylanase I of Aeromonas caviae ME-1 isolated from the intestine of a			
RT	herbivorous insect (Samia cynthia pryeri)."			
RL	Biosci. Biotechnol. Biochem. 56:1463-1464(1992).			
RP	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=ME-1; TISSUE=Gut content of silk worm;			
RA	Suzuki T., Itoh Y., Naito H., Kubata K.B., Horitsu H., Takamizawa K.,			
RA	Kawai K.;			
RT	"Molecular cloning of the xynA gene encoding an endo-xylanase (xylanase			
RT	I) of Aeromonas caviae ME-1.;"			
RL	Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; D32065; BAA06837.1; -; Genomic_DNA.			
DR	HSSP; P09850; 1XNB.			
DR	SMR; Q43993; 25-211.			
DR	GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	GO; GO:00045493; P:xyloan catabolism; IEA.			
DR	InterPro; IPR001137; Glyco_hydro_11.			
DR	Pfam; PF00457; Glyco_hydro_11; 1.			
DR	PRINTS; PR00911; GLHYDLASE11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Signal; Xylan degradation.			
FT	SIGNAL	1	28	Potential.
FT	CHAIN	29	211	xylanase I.
EQ	SEQUENCE	211 AA;	23136 MW;	F9E30403BB935E49 CRC64;

Query Match	79.3%	Score 929;	DB 2;	Length 211;
Best Local Similarity	79.3%	Pred. NO. 6.8e-67;		
Matches 169;	Conservative 18;	Mismatches 24;	Indels 2;	Gaps 2;

[illegible]

RESULT 14	
Q171835	BACFI PRELIMINARY; PRT; 210 AA.
ID	Q71835 BACFI PRELIMINARY; PRT; 210 AA.
AC	Q71835
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Xylanase.
OS	Bacillus firmus.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX	NCBI_taxid=1399;
[1]	
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=K-1;
RA	Chuensumran U., Ratanakhanokchai K., Cheevadhanarak S.;
RL	Submitted (OCT-2000) to the EMBL/GenBank/DDSI databases.
ER	EWBL; AF317713; AAQ14588.1; -; Genomic_DNA.
DR	HSP; P09850; 1BCX.
DR	SNR; Q71835; 27-210.
DR	GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glyc
DR	GO; GO:0005975; F:carbohydrate metabolism; IEA.
GO	GO:0045493; P:xylan catabolism; IEA.
DR	InterPro; IPR01137; Glyco hydro 11.
DR	Pfam; PF00457; Glyco hydro 11; 1.
DR	PRINTS; PR00911; GLYDRLASE11.
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW	Xylan degradation.
SO	SEQUENCE 210 AA; 23313 MW; AC4BASDD5D67A1B2 CRC64;

Query Match	73.8%	Score	864.5	DB 2	Length	210
Best Local Similarity	74.2%	Pred. NO.	1.1e-61			
Matches	158	Conservative	19	Mismatches	33	Indels
					3	Gaps
					2	

Qy	1	MF	F	K	N	F	L	V	G	L	S	A	L	M	S	I	S	L	F	S	A	T	A	S	A	S	T	D	Y	Q	N	Q	N	T	D	G	G	I	V	N	A	V	N	G	S	G	N	S	V	N	W	S	N	60	
Db	1	MF	F	V	T	K	V	L	T	V	I	A	A	T	I	S	F	C	L	S	A	V	P	A	S	-	N	T	Y	Q	Y	T	D	G	G	T	V	N	A	T	G	P	G	N	Y	S	V	T	W	R	D	58			
Qy	61	T	G	N	F	V	C	K	G	W	T	T	C	S	P	F	T	I	N	N	A	G	W	A	P	N	G	N	G	Y	L	T	L	Y	C	W	T	S	P	L	E	Y	V	V	D	S	W	G	T	P	T	120			
Db	59	T	G	N	F	V	C	K	G	W	E	I	S	P	N	T	I	I	H	N	A	G	W	B	F	S	G	N	G	Y	L	T	L	Y	C	W	T	R	N	L	E	Y	V	V	D	N	W	G	T	P	T	118			
Qy	121	T	Y	A	G	T	V	K	S	D	G	T	D	I	Y	I	T	T	R	N	A	P	S	I	D	G	R	T	T	F	T	Q	Y	S	V	R	S	K	R	P	T	G	S	N	A	T	I	F	S	N	H	V	N	A	180
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Qy	181	W	K	S	H	M	N	L	G	N	W	A	Y	Q	V	N	A	T	E	G	Y	Q	S	S	S	N	V	T	W	213																									
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RESULT 15
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ID Q9KEF3_BACHD PRELIMINARY; PRT; 210 AA.
AC Q9KEF3;
DT 01-OCT-2000 (TREMblrel. 15. Created)

DT	01-OCT-2000 (TrEMBLrel. 15, last sequence update)	
DT	13-SEP-2005 (TrEMBLrel. 31, last annotation update)	
DE	Endo-1,4-beta-xylanhydrolase.	
GN	Names=xynIIA; OrderedLocusNames=BH0899;	
OS	Bacillus halodurans.	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
OX	NCBI_TaxID=86665;	
OX	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C-125 / JCM 9153;	
RC	MEDLINE=20512562; PubMed=110581132; DOI=10.1093/nar/28.21.4317;	
RX	Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,	
RA	Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kunara S.,	
RA	Horikoshi K.;	
RA	"Complete genome sequence of the alkaliphilic bacterium Bacillus	
RT	halodurans and genomic sequence comparison with Bacillus subtilis.";	
RT	Nucleic Acids Res. 28:4317-4331(2000).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=MIR32;	
RC	MEDLINE=22269261; PubMed=12382115; DOI=10.1007/s00792-002-0269-4;	
RX	Martinez M.A., Delgado O.D., Breccia J.D., Baigori M.D., Sineriz F.;	
RL	Submission (OCT-2002) to the EMBL/GenBank/DBJ databases.	
RL	EMBL; BA000004; BAB04618.1; -; Genomic DNA.	
DR	EMBL; AX170624; AA012276.1; -; Genomic_DNA.	
DR	PIR; C83762; C83762.	
DR	HSSP; P09850; 1XNB.	
DR	SNR; Q9KEF3; 27-210.	
DR	GO; GO:0016787; F:Hydrolase activity; IEA.	
DR	GO; GO:0004573; F:Hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.	
DR	GO; GO:0005955; F:carbohydrate metabolism; IEA.	
DR	InterPro; IPR001137; Glyco hydro 11.	
DR	Pfam; PF00457; Glyco hydro 11.1.	
DR	PRINTS; PR00911; GLHYDRLASE11.	
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_Fil_2; 1.	
KW	Complete proteome; Hydrolase.	
SK	SEQUENCE 210 AA; 23313 MW; AC4BASDD5D67A1B2 CRC64;	
	Query Match 73.8%; Score 864.5; DB 2; Length 210;	
	Best Local Similarity 74.28; Pred. No. 1.e-61;	
	Matches 156; Conservative 19; Mismatches 33; Indels 3; Gaps 2;	
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QY	61 TGNFVVGKWTGSPFTTINYNAGVWAPNGNGYLTLYGWTSPLEIYVVDWSGTYRPTG 120	
DB	59 TGNFVVGKWEIGSPNRTIHYNAGVSPSGNGYLTLYGWTNRQNLIEIYVVDNWGTYRPTG 118	
QY	121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRFTFTQYMSVRSQKPTGSAITTFNSHVNA 180	
DB	119 THRGTVSDGGTYDIYTTMYNARSIDGTQ-TFQQFWSVRSQKPTGNNVSIITFSHVNA 177	
QY	181 WKSHGMNLGSNWAYQVMATEGYQSGSGSNVTW 213	
DB	178 WRNAGMNLGSWSYQVLATEGYQSGSGSNVTW 210	

Search completed: February 3, 2006, 09:17:54
Job time : 109 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:18:52 ; Search time 30 Seconds
(without alignments)
586.997 Million cell updates/sec

Title: US-10-626-583-5
Perfect score: 1171
Sequence: 1 MFKEKQFLVGLSAALMSIS.....YQVMATEGYQSSGSSNTVW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.7	213	2	US-09-570-856B-1
2	1168	99.7	213	2	US-09-570-856B-13
3	1141	97.4	208	1	US-08-315-695-21
4	1130	96.5	213	1	US-08-104-445-3
5	1041	88.9	185	1	US-08-044-621D-37
6	1041	88.9	185	1	US-08-709-912-5
7	1041	88.9	185	1	US-09-047-370-5
8	1038	88.6	185	1	US-08-044-621D-36
9	1038	88.6	185	1	US-08-709-912-3
10	1038	88.6	185	1	US-09-047-370-3
11	987	84.3	185	2	US-09-570-856B-5
12	984	84.0	185	2	US-09-570-856B-9
13	979	83.6	185	2	US-09-570-856B-7
14	977	83.4	185	2	US-09-570-856B-4
15	976	83.3	185	2	US-09-570-856B-6
16	974	83.2	185	2	US-09-570-856B-3
17	955	81.6	185	2	US-09-570-856B-10
18	955	81.6	211	1	US-08-575-964-1
19	955	81.6	211	1	US-08-963-500-1
20	951	81.2	185	2	US-09-570-856B-12
21	933	79.7	185	2	US-09-570-856B-8
22	920	78.6	185	2	US-09-570-856B-11
23	640.5	54.7	189	1	US-08-709-912-13
24	640.5	54.7	189	1	US-09-047-370-13
25	637	54.4	240	2	US-09-570-856B-16
26	636	54.3	344	1	US-08-468-812-2
27	636	54.3	344	2	US-08-590-563-2

28	636	54.3	344	2	US-09-770-621-2	Sequence 2, Appli
29	636	54.3	344	2	US-09-235-832-2	Sequence 2, Appli
30	635	54.2	216	1	US-08-315-695-20	Sequence 20, Appli
31	627.5	53.6	200	1	US-07-744-570B-2	Sequence 2, Appli
32	625.5	53.4	191	1	US-08-044-621D-35	Sequence 35, Appli
33	618.5	52.8	191	1	US-08-709-912-11	Sequence 11, Appli
34	618.5	52.8	191	1	US-09-047-370-11	Sequence 11, Appli
35	594	50.7	206	1	US-08-315-695-19	Sequence 19, Appli
36	594	50.7	215	1	US-08-044-621D-34	Sequence 34, Appli
37	594	50.7	335	2	US-09-570-856B-15	Sequence 15, Appli
38	587	50.1	191	1	US-08-709-912-10	Sequence 10, Appli
39	587	50.1	191	1	US-09-047-370-10	Sequence 10, Appli
40	585.5	50.0	230	2	US-08-768-373-4	Sequence 4, Appli
41	585.5	50.0	230	2	US-08-849-242A-4	Sequence 4, Appli
42	583.5	49.8	225	1	US-08-290-979A-8	Sequence 8, Appli
43	579	49.4	189	1	US-08-044-621D-33	Sequence 33, Appli
44	573.5	49.0	225	2	US-09-570-856B-26	Sequence 26, Appli
45	572	48.8	189	1	US-08-709-912-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-09-570-856B-1
; Sequence 1, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dabivat, Basil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus circulans
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (29)..()
; OTHER INFORMATION:
US-09-570-856B-1

Query Match	99.7%	Score 1168;	DB 2;	Length 213;
Best Local Similarity	99.5%	Pred. No. 6.3e-98;		
Matches 212;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFKEKQFLVGLSAALMSISLFSATAAATDYQNQNTDGGGVNNAVNGSGGNTSVNWSN	60	
Db	1	MFKEKQFLVGLSAALMSISLFSATAAATDYQNQNTDGGGVNNAVNGSGGNTSVNWSN	60	
Qy	61	TGNFVVGKGTGTPFRRTINYNAGVAPNGNGYLYLGVWTRSPLEYVVDVSWGTYRPTG	120	
Db	61	TGNFVVGKGTGTPFRRTINYNAGVAPNGNGYLYLGVWTRSPLEYVVDVSWGTYRPTG	120	
Qy	121	TYKGTVKSDDGTYDIYTTTTRYNAPSIDGRTFTFYQVSVROSQRPTGSGNATITFSNVNA	180	
Db	121	TYKGTVKSDDGTYDIYTTTTRYNAPSIDGRTFTFYQVSVROSQRPTGSGNATITFSNVNA	180	
Qy	181	WKSHGMNLGNSWAYQVMATEGYQSSGSSNTVW	213	
Db	181	WKSHGMNLGNSWAYQVMATEGYQSSGSSNTVW	213	


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RESULT 2
US-09-570-856B-13
; Sequence 13, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570.856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus subtilis
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (29)..()
; OTHER INFORMATION:
US-09-570-856B-13

Query Match          99.7%; Score 1168; DB 2; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.3e-98;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSGGNTSVNWSN 60
Db 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSGGNTSVNWSN 60

Qy 61 TGNFVVGKWTGSPFRTININAGVWAPNGVLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTININAGVWAPNGVLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSGSSNNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSGSSNNVTW 213

RESULT 3
US-08-315-695-21
; Sequence 21, Application US/08315695
; Patent No. 5591619
; GENERAL INFORMATION:
; APPLICANT: Li, Xin-Liang
; APPLICANT: Ljungdahl, Lars G.
; TITLE OF INVENTION: Aureobasidium Pullulans Xylanase, Gene
; TITLE OF INVENTION: and Signal Sequence
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

RESULT 4
US-08-104-445-3
; Sequence 3, Application 08/104445
; Patent No. 5306633
; GENERAL INFORMATION:
; APPLICANT: GOTTSCHALK, MICHAEL
; APPLICANT: SCHUSTER, ERWIN
; APPLICANT: SPROESSLER, BRUNO
; TITLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS
; TITLE OF INVENTION: PRODUCTION, BACTERIA PRODUCING A XYLANASE, DNA FRAGMENT
; TITLE OF INVENTION: ENCODING A XYLANASE, PLASMID CONTAINING THE DNA FRAGMENT,
; TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FO
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/104,445
; FILING DATE:
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5306633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 583-179-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-104-445-3

Query Match      96.5%; Score 1130; DB 1; Length 213;
Best Local Similarity 95.3%; Pred. No. 1.7e-94;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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DB 1 MFKFKFLVLGLTAAFMSISLFSATASAGTDYQWQNTDGGGINVAVNGSGGNYSVWNSN 60
QY 61 TGNFVVGKGTGTPSPRINTYNAGYVAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
DB 61 TGNFVVGKGTGTPSPRINTYNAGYVAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
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DB 121 TYGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
QY 181 WKSHGMNLGNWAYQVMATEGYQSSGSSNVTVM 213
DB 181 WKSHGMNLGNWAYQVMATEGYQSSGSSNVTVM 213

RESULT 5
US-08-044-621D-37
; Sequence 37, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Wakarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Gowling, Strathy & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1C3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,621D
; FILING DATE: April 8, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy A. Erratt
; REGISTRATION NUMBER: 34,076
; REFERENCE/DOCKET NUMBER: 08-863796
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 613-786-0199
; TELEFAX: 613-563-9869
; TELEX:
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185
; TYPE: Amino Acid
; STRANDEDNESS: No. 5405769 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus subtilis
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; AUTHORS: Paice M.G., Bourbonnais R., Desrochers
; AUTHORS: M., Jurasek L., & Yaguchi M.
; TITLE:
; JOURNAL: Arch. Microbiol.
; VOLUME: 144
; ISSUE:
; PAGES: 201-206
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-044-621D-37

Query Match      88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ASTDYQWQNTDGGGINVAVNGSGGNYSVWNSNTGNFVVGKGTGTPSPRINTYNAGVWAP 88
DB 1 ASTDYQWQNTDGGGINVAVNGSGGNYSVWNSNTGNFVVGKGTGTPSPRINTYNAGVWAP 60
QY 89 NNGYLYLYGWTRSPLEIYYVVDVSWGTYRPTGTYGTVKSDGGTYDIYTTTRYNAPSIDG 148
DB 61 NNGYLYLYGWTRSPLEIYYVVDVSWGTYRPTGTYGTVKSDGGTYDIYTTTRYNAPSIDG 120
QY 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKSHGMNLGNWAYQVMATEGYQSSGSS 208
DB 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKSHGMNLGNWAYQVMATEGYQSSGSS 180
QY 209 NVTVM 213
DB 181 NVTVM 185

RESULT 6
US-08-709-912-5
; Sequence 5, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
```

COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORGANISM: Bacillus subtilis
AUTHORS: Parce, M.G.
AUTHORS: Bourbonnais, R
AUTHORS: Desrochers, M
AUTHORS: Jurasek, L
AUTHORS: Yaguchi, M
JOURNAL: Arch. Microbiol.
VOLUME: 144
PAGES: 201-206
DATE: 1986
US-08-709-912-5
Query Match 88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTINYNAGVWAP 88
DB 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTINYNAGVWAP 60
QY 89 NNGYLLTYLGTWTRSPLEIYYVVDVSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
DB 61 NNGYLLTYLGTWTRSPLEIYYVVDVSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120
QY 149 DRTTFTQWVSQRKPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYOSSGSS 208
DB 121 DRTTFTQWVSQRKPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYOSSGSS 180
QY 209 NVTVM 213
DB 181 NVTVM 185

RESULT 7
US-09-047-370-5
Sequence 5, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORGANISM: Bacillus subtilis
AUTHORS: Parce, M.G.
AUTHORS: Bourbonnais, R
AUTHORS: Desrochers, M
AUTHORS: Jurasek, L
AUTHORS: Yaguchi, M
JOURNAL: Arch. Microbiol.
VOLUME: 144
PAGES: 201-206
DATE: 1986
US-09-047-370-5
Query Match 88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTINYNAGVWAP 88
DB 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTINYNAGVWAP 60
QY 89 NNGYLLTYLGTWTRSPLEIYYVVDVSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
DB 61 NNGYLLTYLGTWTRSPLEIYYVVDVSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120
QY 149 DRTTFTQWVSQRKPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYOSSGSS 208
DB 121 DRTTFTQWVSQRKPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYOSSGSS 180
QY 209 NVTVM 213
DB 181 NVTVM 185

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RESULT 8
US-08-044-621D-36
; Sequence 36, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Wakarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gowling, Strathy & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1C3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 in., 360kB storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,621D
; FILING DATE: April 8, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy A. Erratt
; REGISTRATION NUMBER: 34,076
; REFERENCE/DOCKET NUMBER: 08-863796
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 613-786-0199
; TELEFAX: 613-563-9869
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185
; TYPE: Amino Acid
; STRANDEDNESS: No. 5405769 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus circulans
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; AUTHORS: Yang R.C.A., Mackenzie C.R. & Narang
; AUTHORS: R.A.
; TITLE:
; JOURNAL: Nucleic Acids Res.
; VOLUME: 16
; ISSUE:
; PAGES: 7187
; DATE: 1988
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-36

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Query Match 88.6%; Score 1038; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 3e-86;

Matches	184;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	29	ASTDYQWQNTDGGI	VNAVNGSGGNYSVNWSNTGNFVVGKGTGSPFRTINYNAGVWAP	88					
Db	1	ASTDYQWQNTDGGI	VNAVNGSGGNYSVNWSNTGNFVVGKGTGSPFRTINYNAGVWAP	60					
QY	89	NGNGYLTLTGWTRSP	LIIEYVVVDSWCTYPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG	148					
Db	61	NGNGYLTLTGWTRSP	LIIEYVVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDG	120					
QY	149	DRITFTQYWSVRQSKR	PTGSNATINPFSNNHVNAAKSHGMNLGSNWAYQVMATEGYQSSGSS	208					
Db	121	DRITFTQYWSVRQSKR	PTGSNATITFTNNHVAKSHGMNLGSNWAYQVMATEGYQSSGSS	180					
QY	209	NVTWV	213						
Db	181	NVTWV	185						

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RESULT 9
US-08-709-912-3
; Sequence 3, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Iehikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Bacillus circulans
; PUBLICATION INFORMATION:
; AUTHORS: Yang, R.C.A.
; AUTHORS: Mackenzie, C.R.
; AUTHORS: Narang, S.A.
; JOURNAL: Nucleic Acid Research
; VOLUME: 16
; PAGES: 7187

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JOURNAL: NU
VOLUME: 16
PAGES: 7187

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f
US-08-709-912-3
DATE: 1988
Query Match 88.6%; Score 1038; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 3e-86;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGMLGNSWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFTNHVNAWSHGMLGNSWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 10
US-09-47-370-3
; Sequence 3, Application US/09047370
; Patent No. 5866408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/709,912
; FILING DATE: 09-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:

; ORGANISM: Bacillus circulans
; PUBLICATION INFORMATION:
; AUTHORS: Yang, R.C.A.
; AUTHORS: MacKenzie, C.R.
; JOURNAL: Nucleic Acid Research
; VOLUME: 16
; PAGES: 7187
; DATE: 1988
US-09-047-370-3

Query Match 88.6%; Score 1038; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 3e-86;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGMLGNSWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFTNHVNAWSHGMLGNSWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 11
US-09-570-856B-5
; Sequence 5, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Basil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570.856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-5

Query Match 84.3%; Score 987; DB 2; Length 185;
Best Local Similarity 94.6%; Pred. No. 1.2e-81;
Matches 175; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGMLGNSWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFTNHVNAWSHGMLGNSWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
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Db 181 NVTW 185

RESULT 12
US-09-570-856B-9
; Sequence 9, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-9

Query Match 84.0%; Score 984; DB 2; Length 185;
Best Local Similarity 93.5%; Pred. No. 2.3e-81;
Matches 173; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPRTTINYNAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPRTTINYNAGVWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGTGKVDGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGTGKVDGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 14
US-09-570-856B-4
; Sequence 4, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-4

Query Match 83.4%; Score 977; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 9.8e-81;
Matches 174; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPRTTINYNAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPRTTINYNAGVWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGTGKVDGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGTGKVDGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 15
US-09-570-856B-6
; Sequence 6, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-7

Query Match 83.6%; Score 979; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 6.5e-81;
Matches 174; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPRTTINYNAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTWTTGSPRTTINYNAGVWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGTGKVDGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGTGKVDGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTFTQYWSVRQSKRPTGSGNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 13
US-09-570-856B-7
; Sequence 7, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-7

Query Match 83.6%; Score 979; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 6.5e-81;
Matches 174; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
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! PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-6

Query Match 83.3%; Score 976; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 1.2e-80;
Matches 174; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSTGNTGNFVVGKWTGSPPTINYNAGVWAP 88
Db 1 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSTGNTGNFVVGKWTGSPPTINYNAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDGWSGTYRPTGYKGTVKSDGGTYDIYTTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDGWSGTYRPTGYKGTVKSDGGTYDIYTTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSYRQSKRPTGSNATLTFESNHNNAWKSHGNLGSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSYRQSKRPTGSNATLTFESNHNNAWKSHGNLGSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

Search completed: February 3, 2006, 09:19:30
Job time : 30 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2006, 09:23:48 ; Search time 180 Seconds
(without alignments)
494.431 Million cell updates/sec

Title: US-10-626-583-5
Perfect score: 1171
Sequence: 1 MFKKKCNFLVGLSAAALMSIS.....YQVMATEGYQSSGSSNTVTW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	4	US-10-237-386-16
2	1171	100.0	213	5	US-10-626-583-5
3	1171	100.0	213	5	US-10-626-724-5
4	1168	99.7	213	4	US-10-237-386-17
5	1161	99.1	213	5	US-10-626-583-11
6	1161	99.1	213	5	US-10-626-724-11
7	1154	98.5	213	5	US-10-626-583-7
8	1154	98.5	213	5	US-10-626-724-7
9	1149	98.1	213	5	US-10-626-583-9
10	1149	98.1	213	5	US-10-626-724-9
11	1130	96.5	213	5	US-10-626-583-3
12	1130	96.5	213	5	US-10-626-724-3
13	1041	88.9	185	4	US-10-307-441-5
14	1041	88.9	185	4	US-10-237-386-1
15	1041	88.9	185	6	US-11-088-725A-32
16	1041	88.9	197	4	US-10-442-148A-10
17	1041	88.9	360	4	US-10-442-148A-11
18	1038	88.6	185	4	US-10-307-441-3
19	1038	88.6	185	6	US-11-088-725A-30
20	929	79.3	211	4	US-10-237-386-19
21	907.5	77.5	211	4	US-10-237-386-18
22	885	75.6	185	6	US-11-018-645-2
23	885	75.6	185	6	US-11-018-645-14
24	826.5	70.6	192	6	US-11-018-645-8
25	825	70.5	186	6	US-11-018-645-16
26	686.5	59.6	197	6	US-11-018-645-4
27	686.5	59.6	198	6	US-11-018-645-18

28	663.5	56.7	241	4	US-10-237-386-43	Sequence 43, Appl
29	659	56.3	240	4	US-10-237-386-42	Sequence 42, Appl
30	646	55.2	242	4	US-10-237-386-41	Sequence 41, Appl
31	645.5	55.1	239	4	US-10-237-386-40	Sequence 40, Appl
32	640.5	54.7	189	4	US-10-307-441-13	Sequence 13, Appl
33	640.5	54.7	189	6	US-11-088-725A-40	Sequence 40, Appl
34	636	54.3	344	3	US-09-770-621-2	Sequence 2, Appl
35	636	54.3	344	4	US-10-286-993-2	Sequence 2, Appl
36	627.5	53.6	191	6	US-11-088-725A-44	Sequence 44, Appl
37	622	53.1	228	4	US-10-237-386-39	Sequence 39, Appl
38	621	53.0	240	4	US-10-237-386-38	Sequence 38, Appl
39	618.5	52.8	191	4	US-10-307-441-11	Sequence 11, Appl
40	618.5	52.8	191	6	US-11-088-725A-39	Sequence 39, Appl
41	617.5	52.7	234	4	US-10-213-990-69	Sequence 69, Appl
42	587	50.1	191	4	US-10-307-441-10	Sequence 10, Appl
43	587	50.1	191	6	US-11-088-725A-38	Sequence 38, Appl
44	581	49.6	225	4	US-10-237-386-36	Sequence 36, Appl
45	573.5	49.0	189	4	US-10-307-441-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-237-386-16
; Sequence 16, Application US/10237386
; Publication No. US2003018089SA1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; FILE REFERENCE: 674509-2046
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-16

Query Match 100.0%; Score 1171; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFKKKCNFLVGLSAAALMSISLFSATASAASTDYQNVWTDGGGINVAVNGSGNYSVNWNSN	60
Db	1	MFKKKCNFLVGLSAAALMSISLFSATASAASTDYQNVWTDGGGINVAVNGSGNYSVNWNSN	60
Qy	61	TGNFVVGKGTGTGSPFRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDSSWGTYRPTG	120
Db	61	TGNFVVGKGTGTGSPFRTINTNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDSSWGTYRPTG	120
Qy	121	TYKGTFTVKSDDGTYDIYTTTTRYNAPSIDGRTTFTQYWSVROSQRPTGSNATITFNSHNVA	180
Db	121	TYKGTFTVKSDDGTYDIYTTTTRYNAPSIDGRTTFTQYWSVROSQRPTGSNATITFNSHNVA	180
Qy	181	WKSHGMILGNSWAVQVMATEGYQSSGSSNTVTW	213
Db	181	WKSHGMILGNSWAVQVMATEGYQSSGSSNTVTW	213

RESULT 2

US-10-626-583-5
; Sequence 5, Application US/10626583


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; Sequence 11, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-11

Query Match          99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVVDSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 7
US-10-626-583-7
; Sequence 7, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-7

Query Match          98.5%; Score 1154; DB 5; Length 213;
Best Local Similarity 98.1%; Pred. No. 4.9e-95;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVVDSWGTYRPTG 120

; Sequence 11, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-11

Query Match          99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVVDSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 6
US-10-626-724-11
; Sequence 11, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-11
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Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSQKPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSQKPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 8

US-10-626-724-7
; Sequence 7, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBSEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-7

Query Match 98.5%; Score 1154; DB 5; Length 213;
Best Local Similarity 98.1%; Pred. No. 4.9e-95;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSQKPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSQKPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 9

US-10-626-583-9
; Sequence 9, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBSEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132

; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-9

Query Match 98.1%; Score 1149; DB 5; Length 213;
Best Local Similarity 97.7%; Pred. No. 1.4e-94;
Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLIEYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSQKPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSQKPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 10

US-10-626-724-9
; Sequence 9, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBSEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic


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; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-307-441-5

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQWVSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQWVSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-10-237-386-1
; Sequence 1, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-1

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQWVSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQWVSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
```

```

RESULT 15
US-11-088-725A-32
; Sequence 32, Application US/11088725A
; Publication No. US20050214410A1
; GENERAL INFORMATION:
; APPLICANT: Iogen Bio-Products Corporation
; APPLICANT: White, Theresa C
; APPLICANT: Giroux, Genevieve R
; APPLICANT: Wallace, Katie E.A.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
; FILE REFERENCE: Q80712
; CURRENT APPLICATION NUMBER: US/11/088,725A
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,061
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-088-725A-32
```

```

Query Match      88.9%; Score 1041; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQWVSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQWVSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
```

Search completed: February 3, 2006, 09:28:57
Job time : 180 secs

Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 2

US-11-170-653-16

Sequence 16, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 16

LENGTH: 213

TYPE: PRT

ORGANISM: Bacillus subtilis

US-11-170-653-16

Query Match 100.0%; Score 1171; DB 7; Length 213;

Best Local Similarity 100.0%; Pred. No. 7.6e-96;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180

Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 3

US-10-517-939-224

Sequence 224, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Steer, Brian

APPLICANT: Callen, Walter

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Wu, Di

APPLICANT: Blum, David

APPLICANT: Esteeghalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM

FILE REFERENCE: 56462007901

CURRENT APPLICATION NUMBER: US/10/517,939

CURRENT FILING DATE: 2004-12-13

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180

Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 4

US-11-170-653-17

Sequence 17, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 17

LENGTH: 213

TYPE: PRT

ORGANISM: Bacillus circulans

US-11-170-653-17

Query Match 99.7%; Score 1168; DB 7; Length 213;

Best Local Similarity 99.5%; Pred. No. 1.4e-95;

Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60


```
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-170-653-1

Query Match      88.9%; Score 1041; DB 7; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.5e-84; Indels 0; Gaps 0;
Matches 185; Conservative 0; Mismatches 0;

Qy 29 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGGYLTYGWTRSPLEIYYVVDWSGTYRPTGTYKGTIVKSDGGYDYITTYRYNAPSIDG 148
Db 61 NNGGYLTYGWTRSPLEIYYVVDWSGTYRPTGTYKGTIVKSDGGYDYITTYRYNAPSIDG 120

Qy 149 DRTTFTQVWSVROSKRPTGNSNATITFNSHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQVWSVROSKRPTGNSNATITFNSHNVAWSHGNNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 8
US-10-517-939-198
; Sequence 198, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-198

Query Match      81.4%; Score 953; DB 6; Length 211;
Best Local Similarity 81.7%; Pred. No. 9e-77;
Matches 174; Conservative 13; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKEKQKMTVILAAATMSFGLF-ATTSSAATDYQWQNTDGGGIVNAVNGSGGNYSVTWQN 59

Qy 61 TGNFVVGKGTGSPRTTINYAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
Db 60 TGNFVVGKGTGSPNRITINYAGVWAPSGNGYLTLYGWTRNALLIYYVVDWSGTYRPTG 119
```

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Qy 121 TYKGTVKSDDGGTYDIYTTTRYNAPSIDGDRTTFTQVWSVROSKRPTGNSNATITFSNHVNA 180
Db 120 TYKGTVTSDDGGTYDIYTTMRHNAPSIDGTQ-TFAQYMSVROSKRATGVNSSITFSNHVNA 178

Qy 181 WKSHGMNLGSNNWAYQVMATEGYQSSGSSNVTVM 213
Db 179 WASKGMNLGSWSYQVLATEGYQSSGSSNVTVM 211

RESULT 9
US-10-517-939-158
; Sequence 158, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-10-517-939-158

Query Match      79.7%; Score 933.5; DB 6; Length 214;
Best Local Similarity 80.4%; Pred. No. 4.6e-75;
Matches 172; Conservative 12; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MFKEKQFLVGLSAAALMS-ISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWS 59
Db 1 MFKLSKKILMVLTLTISMSFSLFAVTAYAASTDYQWQNTDGGGTVNATNGSDGNYSVSWS 60

Qy 60 NTGNFVVGKGTGSPRTTINYAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPT 119
Db 61 NCGNFVVGKGTGSPRTTINYAGVWAPNGNGYLTLYGWTRNALLIYYVVDWSGTYRPT 120

Qy 120 GTYKGTVKSDDGGTYDIYTTTRYNAPSIDGDRTTFTQVWSVROSKRPTGNSNATITFSNHVN 179
Db 121 GTYKGTVTSDDGGTYDIYTTTRTNAPSIDGNNTFTQFWSVROSKRPTGNTITITFSNHVN 180

Qy 180 AWKSHGMNLGSNNWAYQVMATEGYQSSGSSNVTVM 213
Db 181 AWKSGMNLGSNNWAYQVLATEGYQSSGSSNVTVM 214

RESULT 10
US-11-170-653-19
; Sequence 19, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
```



```
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 211
; TYPE: PRT
; ORGANISM: A. caviae
US-11-170-653-19

Query Match      79.3%; Score 929; DB 7; Length 211;
Best Local Similarity 79.3%; Pred. No. 1.le-74;
Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGVNAGVNGSGGNTSVNWSN 60
Db 1 MFKFKKMLTVLLTASMSFGVFAATSSAA-TDYQWNTDGGGVNAGVNGSGGNTSVNQSN 59

Qy 61 TGNFVVGKGTGSPRTTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 60 TGNFVVGKGTGTYTPNRVYNNAGVFAFGSGNGYLTLYGWTRNALLIEYYVVDVDSWGTYRPTG 119

Qy 121 TYGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGNSATITFSNHVNA 180
Db 120 TYGTVNSDGGTYDIYTTTRYNAPSIDGTQ-TFQYWSVRQSKRPTGNSATITFSNHVNA 178

Qy 181 WKSHGNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 179 WPSKGMNLSWSYQVLAATEGYQSSGSSNVTVW 211
```

```
RESULT 11
US-10-517-939-208
; Sequence 208, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
US-10-517-939-208
```

```
Query Match      79.2%; Score 927; DB 6; Length 210;
Best Local Similarity 80.1%; Pred. No. 1.7e-74;
Matches 169; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

Qy 3 KFKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGVNAGVNGSGGNTSVNWSNTG 62
Db 2 KLKKKMLTLLLTASMSFGVFAATSSAA-TDYQWNTDGGGVNAGVNGSGGNTSVNQNSG 60

Qy 63 NFVVGKGTGSPRTTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTGTY 122
Db 61 NFVVGKGSVGSPPNRTINYNAGIWEPSGNGYLTLYGWTRSNLIBIYYVVDVDSWGTYRPTGTH 120

Qy 123 KGTVKSDDGTDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGNSATITFSNHVNAWK 182
Db 121 KGTVNSDGGTYDIYTTTRYNAPSIDGTQ-TFQYWSVRQSKRPTGNSNVSIITFSNHVNAWR 179

Qy 183 SHGNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 SKGNLGSWSYQVLAATEGYQSSGSSNVTVW 210
```

```
RESULT 12
US-11-170-653-18
; Sequence 18, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sribesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Bacillus stearotheophilus
US-11-170-653-18
```

```
Query Match      77.5%; Score 907.5; DB 7; Length 211;
Best Local Similarity 79.2%; Pred. No. 8.6e-73;
Matches 168; Conservative 12; Mismatches 29; Indels 3; Gaps 3;

Qy 3 KFKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGVNAGVNGSGGNTSVNWSNTG 62
Db 2 KLKKKMLTLLLTASMSFGVFAATSSAA-TDYQWNTDGGGVNAGVNGSGGNTSVNQNTG 60

Qy 63 NFVVGKGTGSPRTTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTGTY 122
Db 61 NFVVGKGTGSPNRVINYNAGIWEPSGNGYLTLYGWTRNALLIEYYVVDVDSWGTYRATGNY 120

Qy 123 K-GTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGNSATITFSNHVNAW 181
Db 121 ESGTVNSDGGTYDIYTTTRYNAPSIDGTQ-TFQYWSVRQSKRPTGNSNVSIITFSNHVNAW 179

Qy 182 KSHGNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 RSKGNLGSNWAYQVLAATEGYQSSGSSNVTVW 211
```

```
RESULT 13
US-10-517-939-190
```

```
; Sequence 190, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-190

Query Match 75.7%; Score 886; DB 6; Length 189;
Best Local Similarity 84.0%; Pred. No. 5.8e-71; Indels 0; Gaps 0;
Matches 158; Conservative 11; Mismatches 19;

Qy 26 ASAASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGV 85
Db 2 ALMASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNCGNFVVGKGTGSAATRVYNAGA 61

Qy 86 WAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTGTYKGTGSDGGTYDIYTTTRYNAPS 145
Db 62 FSPSGNGYALYLGWTRNSLIEYYVVDVDSWGTYPRTGTYKGTGSDGGTYDIYTTTRYNAPS 121

Qy 146 IDGRTTFTQYWSVRQSKRPTGNSNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSS 205
Db 122 IDGNNTTFTQYWSVRQSKRPTGNTTITFSNHVNAWKGHNLGSSWSYQVLATEGYQSS 181

Qy 206 GSSNVTVW 213
Db 182 GYSNVTVW 189

RESULT 14
US-10-517-939-252
; Sequence 252, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; US-10-517-939-252
```

```
; SEQ ID NO 252
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-252

Query Match 74.6%; Score 873.5; DB 6; Length 184;
Best Local Similarity 83.2%; Pred. No. 7e-70; Indels 1; Gaps 1;
Matches 153; Conservative 15; Mismatches 15;

Qy 30 STDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGVWAPN 89
Db 2 ATDYQNWTDGGGIVNAVNGSGGNYSVTWQNSGDFVVGKGSVPRTTINYNAGIWEPS 61

Qy 90 GNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTGTYKGTGSDGGTYDIYTTTRYNAPSIDGD 149
Db 62 GNGYLTLYGWTRNSLIEYYVVDVDSWGTYPRTGTHKGTVNSDGGTYDIYTTMYNAPSIDGT 121

Qy 150 RTTFTQYWSVRQSKRPTGNSNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSSGSSN 209
Db 122 Q-TFQQFWSVRQSKRPTGNSNITFSNHVNAWRSGHNLGSSWSYQVLATEGYQSSGSRN 180

Qy 210 VTVW 213
Db 181 VTVW 184

RESULT 15
US-10-517-939-380
; Sequence 380, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 380
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated polypeptide.
; US-10-517-939-380

Query Match 72.1%; Score 844; DB 6; Length 189;
Best Local Similarity 81.4%; Pred. No. 2.8e-67; Indels 0; Gaps 0;
Matches 153; Conservative 10; Mismatches 25;

Qy 26 ASAASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGV 85
Db 2 ALMASTFYWHNTDGGIVNATNGSDGNYSVSWNSCGNFVVGKGTGSAATRVYNAGA 61

Qy 86 WAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYPRTGTYKGTGSDGGTYDIYTTTRYNAPS 145
Db 62 FSPVGNAYLALYLGWTRNSLIEYYVVDVDSWGTYPRTGTYKGTGSDGGTYDIYTTTRYNAPS 121

Qy 146 IDGRTTFTQYWSVRQSKRPTGNSNATITFSNHVNAWKGHNLGNSNWAYQVMATEGYQSS 205
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Db 122 IDGNNTFTQFWSVRQSKRPICGNTNTTIFSNHVAWAKSGKGNLGSWSYQVLATEGYQSS 181

Qy 206 GSSNVTW 213

Db 182 GYSNVTW 189

Search completed: February 3, 2006, 09:24:52
Job time : 11 secs

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